TITLE:

NON-NUCLEIC ACID PROBES, PROBE SETS, METHODS AND KITS PERTAINING TO THE DETECTION OF HUMAN CHROMOSOMES X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18

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CERTIFICATION UNDER 37 CFR 1.10

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Title Of The Invention:

Non-Nucleic Acid Probes, Probe Sets, Methods And Kits Pertaining To The Detection Of Human Chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18.

Cross Reference to Related Applications:

This application claims the benefit of U.S. Provisional Application No. 60/094,874 filed on July 31, 1998, U.S. Provisional Application No. 60/109,313 filed on November 20, 1998; US Provisional Application No. 60/120,827 filed on February 19, 1999; U.S. Provisional Application No. 60/137,636 filed on June 4, 1999 and U.S. Patent Application No. 09/363,632 filed on July 29, 1999.

Background of the Invention:

1. Field of the Invention

This invention is related to the field of probe-based detection, analysis and quantitation of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18 using detectable non-nucleic acid probes.

2. Description of the Related Art

Nucleic acid hybridization is a fundamental process in molecular biology. Probe-based assays are useful in the detection, identification, analysis and quantitation of nucleic acids. Nucleic acid probes have long been used to analyze samples for the presence of nucleic acid from bacteria, eucarya, fungi, virus or other organisms and they are also useful in examining samples for genetically-based disease states or clinical conditions of interest.

Chromosome disorders comprise a significant number of genetic diseases. For example, approximately 16 percent of recessive disorders are the result of X-linked genetic defects for which no specific diagnostic procedure is presently available (See: Delhanty et al. *Human Mol. Genetics* 2: 1183-1185 (1993)). It has been estimated that detectable chromosomal abnormalities occur with a frequency of one in every 250 births (See: Epstein, The consequency of chromosome imbalance: principle, mechanism and models, Cambridge University Press, 1986; Lubs et al., *Science, 169*: 495-497 (1970); and Jacobs, *Am. J. Epidemiol. 105*: 180-191 (1970)). Abnormalities

which involve the deletion or addition of chromosomal materials after the genetic balance of an organism has been determined can lead to serious mental or physical disease and even death. With the arrival, acceptance and rapid proliferation of in-vitro fertilization (IVF), research into methods and compositions suitable for the examination of the chromosomes of ova, spermatozoa, embryo and blastomeres have become commonplace. For example, recent reports have shown increased incidence of hyperhaplloid (24/XY) spermatozoa in males with 46 XY/47 XXY karyotypes (See: Cozzi et al, *Hum. Genet., 93*: 32-34 (1994); Chevret et al. *Hum. Genet. 97*: 171-175 (1996); Martini et al., *Human Reproduction, 11*: 1638-1643 (1996) and Estop et al., *Human Reproduction, 13*: 124-127 (1998)). For families affected by sex linked disorders, preimplantation diagnosis (PID) is essential to insure that the fetus is not affected. Thus, the examination of blastomeres for sex determination and chromosome disorder prior to implantation has become a routine part of the IVF processes since implantation of chromosomally defective embryos will result in either miscarriage or in the birth of an infant having a genetic defect (See: Harper, *Journal of Assisted Reproduction and Genetics, 13*: 90-95 (1996).

Pioneering work directed to preimplantation and prenatal sex determination was performed by Handyside and his colleagues (See: Handyside et al., *The Lancet*, 347-349 (February, 1989) and Handyside et al., *Nature, 344*: 768-770 (1990)). Handyside et al. used PCR to amplify repetitive satellite sequences of the Y-chromosome. This method was at first very attractive since results could be rapidly obtained (approximately 3 hours). Speed is a critical factor in preimplantation diagnosis since implantation can only occur within a short time when the female uterus is suitable to impregnation. Because only the Y-chromosome was detected, the PCR method developed by Handyside et al. predicted a male child when amplification occurred and a female child when no amplification occurred. However, this method had a rather high incidence of misdiagnosis of prenatal and preimplantation sex determination (See: Kontogianni et al., *Preimplantation Genetics*, Plenum Press, New York, pp. 139-145).

Though improvements were made to the PCR technique to allow for the simultaneous and more accurate detection of X and Y chromosomes (See: Chong et al., *Hum. Mol. Genetics*, 2: 1187-1191: (1993) and Strom et al., *J. of in Vitro Fertilization and Embryo Transfer, 8*: 225-229 (1991)), chromosomal disorders such as aneuploidy (including XXY and XYY karyotypes) and polyploidy were not detectable by improved PCR methods since the methods could not quantitate X and Y chromosomes but merely determine their presence or absence. Furthermore, PCR techniques are highly susceptible to misdiagnosis caused by small amounts of foreign (contaminating) DNA (See: Harper et al., *Hum. Reproduction, 9*: 721-724 (1994)).

Given the limitations of PCR, particularly with regard to misdiagnosis or non-diagnosis of aneuploidy and polyploidy conditions, in-situ hybridization (ISH), and particularly fluorescence in-situ hybridization (FISH), has become another used and often preferred method for the analysis of cells, tissues (including bone marrow), spermatozoa, ova, blastomeres, oocysts, buccal cells and chorinic ville. ISH and FISH can be used to examine both metaphase chromosome spreads and interphase nuclei. Because intracelluar chromosomes are routinely visualized (examined) within the nuclei or metaphase condition, the exact number of chromosomes per cell can be quantitated. Therefore, abnormal conditions such as aneuploidy and polyploidy are easily diagnosed. While FISH techniques have become established in clinical and medical applications utilizing nucleic acid probes, typically its Achilles Heal has been that the procedure is often slow to yield results as compared with PCR techniques.

Long arrays of tandemly repeated satellite DNAs are known to exist in the human genome and can generally be organized into distinct classes (See: Greig et al., *Am. J. Hum. Genet., 45:* 862-872 (1989). However, subsets of the satellite DNA classes appear to have evolved such that they are largely specific to the chromosome of origin. Thus, alpha satellite DNAs provide chromosome specific markers which can be used as a basis of individual chromosome identification. However, there is a possibility that these markers exist in low abundance on other chromosomes (See: Greig et al., *Am. J. Hum. Genet., 45:* 862-872 (1989) at p. 865, col. 2, lns. 6-15).

ISH and FISH based chromosome analysis is typically performed using DNA probes which are greater than 100 bp in length (often greater than a kb in length), which typically have multiple labels and which are directed to target sequences of alpha satellite DNA of the chromosome sought to be detected. These probes are typically generated by digestion of naturally occurring DNAs (nick translation) or by enzymatic synthesis using naturally occurring DNA as a template. Thus the probes are typically a heterogeneous population of numerous fragments, the exact composition of which varies substantially from preparation to preparation. Consequently, the performance of the probes will typically vary from preparation to preparation.

Particularly when utilized in the same assay under a single set of stringency conditions, these nucleic acid probes (composition of nucleic acid fragments) may exhibit some cross reaction to other chromosomes of the sample (See: Matera et al., *Genomics, 18*: 729-731 (1993)). Cross reaction is at least partially the result of the strong sequence homology within the classes of alpha satellite DNA and thereby requires that the assay exhibit a high degree of

discrimination for long DNA probes under preset conditions of stringency. Thus, typical oligonucleotide probes can exhibit cross reaction at, what is commonly referred to as, both low and even high stringency conditions. Since cross hybridization occurs under conditions of both low and high stringency, the signal to noise ratio is poor for these assays regardless of the nature of the stringency conditions. This is particularly disadvantageous for multicolor analysis wherein different fluorophores can exhibit different efficiencies for signal generation. Cross reaction can also be particularly disadvantageous in an assay which is automated since these processes often will mis-call weak signals as false positives.

A commonly used method for reducing cross reaction caused by non-specific hybridization in *in-situ* hybridization assays involves the use of "blocking nucleic acid" (See: Gray et al., US 5,447,841). Common sources of blocking nucleic acid can include enzymatically digested DNA, salmon sperm DNA as well as other natural sources of heterogenous nucleic acid. Similarly, synthetic oligonucleotides can be used to reduce the binding of probes to non-target sequences though this methodology does not appear to have been utilized in chromosome analysis (See: Arnold et al., US 5,434,047). Likewise, PNA probes have been used to suppress the binding of detectable probes to non-target sequences though again this methodology has not been previously applied to chromosome analysis (See: WIPO Patent Application: WO98/24933).

As applied to the analysis of chromosomes X and Y, ISH and FISH techniques have typically employed DNA probes which have multiple labels and which are typically greater than 100 base pairs (bp) in length and which are prepared by nick translation of cloned DNA greater than 1 kilobase (kb) in length (See: Chevet et al, *Hum. Genet., 97*: 171-175 (1996)). The most commonly used probes for analysis of sex disorders appear to be commercially available sets of probes CEP X/Y/18/13/21 (See: Munne et al., *Human Reproduction, 8*: 2185-2191 (1993)) which are available from Vysis, (formerly Imagenetics) or similar DNA probes which are available from Oncor (See: Martini et al., *Human Reproduction, 11*: 1638-1643 (1996)). Generally, the DNA probes for the analysis of X and Y are directed to target sequences of alpha satellite DNA of the chromosome sought to be detected.

As applied to the analysis of human chromosome 2, ISH and FISH techniques have typically employed nick translated DNA probes which have multiple labels and which are greater than 100 base pairs (bp) in length (See: Haaf et al., *Genomics, 13*: 122-128 (1992) referencing Greig et al., *Am. J. Hum. Genet., 45:* 862-872 (1989). Similarly, the FISH analysis of human chromosome 10 was performed using nick translated DNA probe or approximately 175 bp (See: Howe et al., *Hum. Genet. 91:* 199-204 (1993). Methods and sequence information suitable

for producing, by digestion of chromosomal DNA or by nick translation, long DNA probes suitable for the analysis of human chromosome 6 can be found in Jabs et al., *Am. J. Hum. Genet. 41:* 374-390 (1997).

As applied to the analysis of chromosome 16, ISH and FISH techniques have typically employed nick translated DNA probes which have multiple labels and which are greater than 100 base pairs (bp) in length (See: Greig et al., *Am. J. Hum. Genet., 45:* 862-872 (1989) and Stallings et al., *Genomics, 13:* 332-338 (1992)). However, Stallings et al., did utilize a synthetic 35-mer for the identification and characterization of CH16LAR (lies on chromosome 16) sequences though this was not an ISH or FISH assay (See: Stallings et al., *Genomics, 13:* 332-338 (1992) at the section entitled "Identification And Characterization Of CH16LAR Sequences" beginning p. 336, col. 1). A PCR assay has been developed to assay chromosome 16 for loss of hyterozygosity though this is not a probe-based assay (See: Kihana et al., *Jpn. J. Cancer Res., 87:* 1184-1190 (1996). Analysis of alpha satellite DNA of chromosomes 17 and 18 have utilized DNA probes of hundreds to thousands of nucleotides in length (See: Waye et al, *Molecular and Cellular Biology, 6:* 3156-3165 (1986) and Alexandrov et al., *Genomics 11:* 15-23 (1991), respectively).

The methods thus far described all relate to the analysis of chromosomes X, Y, 1, 2, 6, 10 16, 17 or 18 using conventional nucleic acid based assay formats. However, the FISH analysis of human chromosome 5 has been described using a 30-mer synthetic oligonucleotide probe (See: Matera et al., *Genomics, 18:* 729-731 (1993) directed to the centromeric region. This is the only example, of which Applicant is aware, of using a synthetic nucleic acid in a FISH format to identify a human chromosome.

Despite its name, Peptide Nucleic Acid (PNA) is neither a nucleic acid, a peptide nor is it even an acid. Peptide Nucleic Acid (PNA) is a non-naturally occurring polyamide which can hybridize to nucleic acid (DNA and RNA) with sequence specificity (See United States Patent No. 5,539,082 and Egholm et al., *Nature 365*:566-568 (1993)). Being a non-naturally occurring molecule, unmodified PNA is not known to be a substrate for the enzymes which are known to degrade peptides or nucleic acids. Therefore, PNA should be stable in biological samples, as well as have a long shelf-life. Unlike nucleic acid hybridization which is very dependent on ionic strength, the hybridization of a PNA with a nucleic acid is fairly independent of ionic strength and is favored at low ionic strength, conditions which strongly disfavor the hybridization of nucleic acid to nucleic acid (Egholm et al., *Nature*, at p. 567). The effect of ionic strength on the stability and conformation of PNA complexes has been extensively investigated (Tomac et al., *J. Am. Chem. Soc. 118*: 5544-5552 (1996)). Sequence discrimination is more efficient

for PNA recognizing DNA than for DNA recognizing DNA (Egholm et al., *Nature*, at p. 566). However, the advantages in point mutation discrimination with non-nucleic acid probes, as compared with DNA probes, in a hybridization assay, appears to be somewhat sequence dependent (Nielsen et al., *Anti-Cancer Drug Design 8*:53-65, (1993) and Weiler et al., *Nucl. Acids Res. 25:* 2792-2799 (1997)).

Though they hybridize to nucleic acid with sequence specificity (See: Egholm *et al.*, *Nature*, at p. 567), PNAs have been slow to achieve commercial success at least partially due to cost, sequence specific properties/problems associated with solubility and self-aggregation (See: Bergman, F., Bannwarth, W. and Tam, S., *Tett. Lett. 36*:6823-6826 (1995), Haaima, G., Lohse, A., Buchardt, O. and Nielsen, P.E., *Angew. Chem. Int. Ed. Engl. 35*:1939-1942 (1996) and Lesnik, E., Hassman, F., Barbeau, J., Teng, K. and Weiler, K., *Nucleosides & Nucleotides 16*:1775-1779 (1997) at p 433, col. 1, ln. 28 through col. 2, ln. 3) as well as the uncertainty pertaining to non-specific interactions which might occur in complex systems such as a cell (See: Good, L. et al., *Antisense & Nucleic Acid Drug Development 7*:431-437 (1997)). Consequently, their unique properties clearly demonstrate that PNA is not the equivalent of a nucleic acid in either structure or function. Thus, PNA probes need to be evaluated for performance and optimization to thereby confirm whether they can be used to specifically and reliably detect a particular nucleic acid target sequence, particularly when the target sequence exists in a complex sample such as a cell, tissue or organism.

PNA probes have been demonstrated as being useful for the detection of rRNA in ISH and FISH assays (See: WO95/32305 and WO97/18325). PNA probes have also been used in the analysis of mRNA (e.g. Kappa Light Chain), viral nucleic acid (e.g. human papillomavirus) and the analysis of centromeric sequences in human chromosomes. Importantly, a PNA probe has also been used to detect human X chromosome specific sequences in a PNA-FISH format (See: WO97/18325).

The analysis of the telomere length of human chromosomes has been demonstrated using PNA probes in a FISH assay (See: Lansdorp et al., Human Mol. Genetics, 5: 685-691 (1996) as well as WO97/14026). Telomere length was measurable since the intensity of fluorescence from the terminus of the chromosome was shown to be proportional to the number of hybridized PNA probes and therefore proportional to the length of the telomere.

Similarly, the analysis of trinucleotide repeats in chromosomal DNA using appropriate PNA probes has been suggested (See: WO97/14026). Subsequently, DNA and PNA probes were used to examine cells for genetic defects associated with expansion of trinucleotide repeats

which manifest as the disease known as human myotonic dystrophy (See: Taneja, *Biotechniques*, 24: 472-476 (1998)). The molecular basis of myotonic dystrophy (DM) is an extreme expansion of CTG repeat sequences in the 3'-UTR of the transcripts for the myotonin protein kinase (DMPK) gene. The severity and age of onset of this disease is known to be proportional to the length of the repeat expansion. The intensity of fluorescence from PNA probes hybridized to the targeted repeats could be used to quantify the length of the expansion repeat. This suggest the possibility of expansion repeat quantitation in a manner useful to confirm the diagnosis of genetic disease and possibly quantifying the age of onset and anticipated severity of the disease.

The Applicant is unaware of any previously described use of peptide nucleic acid (PNA) probes for the detection, identification or enumeration of chromosomes Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18.

In summary, any methods, kits or compositions which could improve the specificity, sensitivity and reliability of probe-based assays for the detection of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18 would be a useful advance in the state of the art particularly where the methods were uniformly applicable to probes of all or substantially all sequence variations. Moreover, the methods, kits or compositions would be particularly useful if they could provide for the rapid, reliable, accurate, sensitive and automated multiplex analysis of samples for the presence, absence or number of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18. It would be most useful if the methods, kits and compositions were suitable for the simultaneous analysis of some or all of the human chromosomes in the same assay.

Summary of the Invention:

This invention is directed to non-nucleic acid probes, probe sets, methods and kits useful for detecting, identifying and/or quantitating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample. Non-nucleic acid probes include peptide nucleic acid (PNA) probes as well as other probes which comprise an uncharged or positively charged backbone. The non-nucleic acid probes of this invention comprise probing nucleobase sequences which specifically hybridize with target sequences within the human chromosome sought to be detected. The preferred probing nucleobase sequence of the non-nucleic acid probes useful for detecting, identifying and/or quantitating a particular human chromosome are listed in Table 1.

In preferred embodiments, non-nucleic acid probes are organized into a set which is designed to detect, identify or quantitate, individually or together with other chromosomes, each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 which may be present in the sample. In a most preferred embodiment, a probe set is suitable for the specific detection, identification and/or quantitation of the total number of each of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample of interest. Preferably, the probes or probe sets are integrated into a assay used for the simultaneous detection, identidication and/or quantitation of some or all human chromosomes. Most preferably, the assay is an automated PNA-ISH or PNA-FISH assay.

This invention is further directed to a method suitable for detecting, identifying and/or quantitating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 which may be present in the sample. The method comprises contacting the sample with one or more non-nucleic acid probes, wherein suitable probes are described herein. According to the method, the presence, absence or number, individually or together with other chromosomes, of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in the sample is then detected, identified and/or quantitated. Detection, identification and/or quantitation of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 is made possible by correlating the hybridization, under suitable hybridization conditions or suitable *in-situ* hybridization conditions, of the probing nucleobase sequence of a non-nucleic acid probe to the target sequence of the chromosome sought to be detected to thereby confirm the presence, absence or quantity of one or more the chromosomes sought to be detected. Furthermore, the method can be multiplexed to provide specific detection, identification and/or quantitation of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a single assay provided that the non-nucleic acid probes for a particular chromosome (X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18) are independently

detectable from probes for the other chromosomes in the assay. In a preferred embodiment, non-nucleic acid probes used to detect each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 are each labeled with one or more independently detectable fluorophores to thereby enable correlation of the presence of signal from a particular fluorophore, or set of fluorophores, with the presence of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18. Preferably, the assay is used for the simultaneous detection of all human chromosomes (a multiplex assay) and most preferably the assay is an automated PNA-FISH assay. Most preferably, the assay is automated and performed using either a slide scanner based analysis system, microscope and camera (e.g. CCD camera) or a flow cytometer.

In yet another embodiment, this invention is directed to kits suitable for performing an assay which detects the presence, absence and/or number of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample. The kits of this invention comprise one or more non-nucleic acid probes and other reagents or compositions which are selected to perform an assay or otherwise simplify the performance of an assay. In a preferred embodiment, non-nucleic acid probes of the kit which are used to detect a particular chromosome (X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18) are independently detectable. In a preferred embodiment, different non-nucleic acid probes of the kit are labeled with one or more independently detectable fluorophores to thereby enable correlation of the presence of signal from a particular fluorophore, or set of fluorophores, with the presence of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18. Preferably, the kits are used in an assay suitable for simultaneous detection, idenfication and/or quantitation of some or all human chromosomes and most preferably the assay is an automated PNA-FISH assay. Most preferably, the assay is automated and performed using either a slide scanner based analysis system, microscope and camera (e.g. CCD camera) or a flow cytometer.

In still another embodiment, this invention is directed to a multiplex assay suitable for detecting, identifying and/or enumerating at least two different human chromosomes in the same sample and in the same assay using least two non-nucleic acid probes which are independently detectable. In preferred embodiments, each of the two or more probes can detect the presence, absence and/or number of one of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in the same sample and in the same assay. Preferably, the multiplex assay is a PNA-ISH or PNA FISH assay.

In still one more embodiment, this invention is directed to non-nucleic acid probes comprising two or more linked independently detectable moieties wherein the combination of

the two or more independently detectable moieties is used to identify a particular probe/target sequence hybrid since the combination of the two or more linked moieties is unique. Preferably, the independently detectable moieties are independently detectable fluorophores.

The non-nucleic acid probes, probe sets, methods and kits of this invention have been demonstrated to be specific for human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18. Moreover, the assays described herein are rapid (with a sample containing fixed cells, the assay can be completed in 90 minutes or less), sensitive, reliable and generally applicable to probes of significantly different nucleobase sequence and variable PNA probe length. Assays can be used to accurately detect, identify and/or quantitate each of the total number of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 present in a sample containing all other human chromosomes. Non-limiting examples of typical samples include cells, tissues (including bone marrow), spermatozoa, ova, blastomeres, oocysts, buccal cells and chorinic ville. Most preferably, the methods, kits and compositions of this invention are suitable for the simultaneous detection, identification and/or quantitation of all human chromosomes in a sample. Most preferably, the assay is automated and performed using either a slide scanner based analysis system, microscope and camera (e.g. CCD camera) or a flow cytometer.

The non-nucleic acid probes, probe sets, methods and kits of this invention can be used to detect or identify chromosome related abnormalities. Non-limiting examples of chromosome related abnormalities which can be detected using this invention include aneuploidy karyotypes and polyploidy karyotypes. Additionally, the non-nucleic acid probes, probe sets, methods and kits of this invention are particularly useful for preimplantation diagnosis, for prenatal screening or for use in clinical diagnostic applications.

Brief Description of the Drawings:

General Note: For Figures 1, 2, 3, 4, 5, 8 and 9, the composite digital image was obtained with each of the blue, green and red filters of a CCD camera attached to a microscope. For Figures 6, 7, 10, 11 and 13-16 the composite digital image was obtained with each of the blue and green filters of a CCD camera attached to a microscope. For Figure 12, the filters are as described in Example 10.

In Figure 1 chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of chromosomes indicate that these cells come from a normal human male.

In Figure 2 chromosomes X and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of chromosomes indicate that these cells come from a normal human female.

In Figure 3 chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The imbalance in detectable chromosomes indicates that these cells come from human having an additional Y-chromosome (47XYY). This is an aneuploidy condition known as trisomy.

In Figure 4 chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The imbalance in detectable chromosomes indicates that these cells come from human having three additional X-chromosomes (49XXXXY). This is an aneuploidy condition known as pentasomy.

In Figure 5 metaphase chromosomes of a human having a condition known as triploid (polyploidy) 69XXY is clearly detectable.

In Figure 6 paired signals for human chromosome 2 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 7 paired signals for human chromosome 6 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 8 both rhodamine (red) and fluorescein (green) labeled PNA probes for chromosome 10 were simultaneously hybridized to the cells in the sample. Therefore, in the composite image, spots which are both green and red appear as white (computer generated color). Pairs of white spots for chromosome 10 are clearly detectable in the visible interphase nuclei and metaphase spreads. The data demonstrates that both the green and red PNA probes of different

sequence hybridize to the same regions of the chromosomal DNA to thereby generate predominately white spots as compared with localized blotches of green and red.

In Figure 9 both rhodamine (red) and fluorescein (green) labeled PNA probes for chromosome 16 were simultaneously hybridized to the cells in the sample. Therefore, in the composite image, spots which are both green and red appear as white (computer generated color). Pairs of white spots for chromosome 16 are clearly detectable in the visible interphase nuclei and metaphase spreads. The data demonstrates that both the green and red PNA probes of different sequence hybridize to the same regions of the chromosomal DNA to thereby generate predominately white spots as compared with localized blotches of green and red.

In Figure 10 paired signals for chromosome 17 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 11 paired signals for chromosome 18 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 12A and 12B the composite digital image was obtained with each of the blue, green, red (pseudo colored orange) and Cy5 (pseudocolored red) filters of a CCD camera attached to a microscope. Chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The cells observed in Figure 12A are from a normal human female (XX,11) and the cells observed in Figure 12B are from a normal human male (XY,11).

In Figure 13, paired signals for human chromosome 3 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 14, paired signals for human chromosome 8 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 15, paired signals for human chromosome 11 are clearly detectable in the visible interphase nuclei and metaphase spreads.

In Figure 16, paired signals for human chromosome 12 are clearly detectable in the visible interphase nuclei and metaphase spreads.

Detailed Description of The Invention

1. Definitions:

a. As used herein, the term "nucleobase" shall include those naturally occurring and those non-naturally occurring heterocyclic moieties commonly known to those who utilize nucleic acid technology or utilize peptide nucleic acid technology to thereby generate polymers which can sequence specifically bind to nucleic acids.

b. As used herein, the term "nucleobase sequence" is any segment of a polymer which comprises nucleobase containing subunits. Non-limiting examples of suitable polymers or polymers segments include oligodeoxynucleotides, oligoribonucleotides, peptide nucleic acids, nucleic acid analogs, nucleic acid mimics, linked polymers or chimeras.

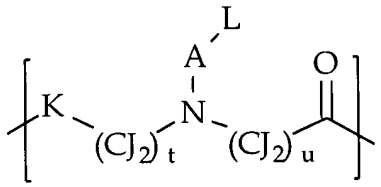
c. As used herein, the term "target sequence" is the nucleic acid sequence of a specific chromosome which is sought to be detected in an assay and to which at least a portion of the probing nucleobase sequence of the chromosome specific non-nucleic acid probe is designed to hybridize.

d. As used herein, the term "non-nucleic acid probe" shall mean a probe comprising a probing nucleobase sequence which is designed to hybridize to at least a portion of the target sequence and is further characterized in that it comprises a neutral or positively charged backbone under suitable hybridization conditions or suitable *in-situ* hybridization conditions. A preferred non-limiting example of a non-nucleic acid probe is a peptide nucleic acid (PNA) probe.

e. As used herein, the term "peptide nucleic acid" or "PNA" shall be defined as any oligomer, linked polymer or chimeric oligomer, comprising two or more PNA subunits (residues), including any of the polymers referred to or claimed as peptide nucleic acids in United States Patent Nos. 5,539,082, 5,527,675, 5,623,049, 5,714,331, 5,736,336, 5,773,571, 5,786,461, 5,837,459, 5,891,625, 5,972,610 and 5,986,053; all of which are herein incorporated by reference. The term "peptide nucleic acid" or "PNA" shall also apply to polymers comprising two or more subunits of those nucleic acid mimics described in the following publications: Diderichsen et al., *Tett. Lett. 37*: 475-478 (1996); Fujii et al., *Bioorg. Med. Chem. Lett. 7*: 637-627 (1997); Jordan et al., *Bioorg. Med. Chem. Lett. 7*: 687-690 (1997); Krotz et al., *Tett. Lett. 36*: 6941-6944 (1995); Lagriffoul et al., *Bioorg. Med. Chem. Lett. 4*: 1081-1082 (1994); Lowe et al., *J. Chem. Soc. Perkin Trans. 1*, (1997) *1*: 539-546; Lowe et al., *J. Chem. Soc. Perkin Trans. 11*: 547-554 (1997); Lowe et al., *J. Chem. Soc. Perkin Trans. 1* 1:5 55-560 (1997); Petersen et al., *Bioorg. Med. Chem. Lett. 6*: 793-

796 (1996); Diederichsen, U., *Bioorganic & Med. Chem. Lett., 8:* 165-168 (1998); Cantin et al., *Tett. Lett., 38:* 4211-4214 (1997); Ciapetti et al., *Tetrahedron, 53:* 1167-1176 (1997); Lagriffoule et al., *Chem. Eur. J., 3:* 912-919 (1997) and the Peptide-Based Nucleic Acid Mimics (PENAMs) of Shah et al as disclosed in WO96/04000.

In preferred embodiments, a PNA is a polymer comprising two or more subunits of the formula:



wherein, each J is the same or different and is selected from the group consisting of H, R^1, OR^1, SR^1, NHR^1, NR^1_2, F, Cl, Br and I. Each K is the same or different and is selected from the group consisting of O, S, NH and NR^1. Each R^1 is the same or different and is an alkyl group having one to five carbon atoms which may optionally contain a heteroatom or a substituted or unsubstituted aryl group. Each A is selected from the group consisting of a single bond, a group of the formula; $-(CJ_2)_s-$ and a group of the formula; $-(CJ_2)_sC(O)-$, wherein, J is defined above and each s is an integer from one to five. The integer t is 1 or 2 and the integer u is 1 or 2. Each L is the same or different and is independently selected from the group consisting of J, adenine, cytosine, guanine, thymine, uridine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, 2,6-diaminopurine, hypoxanthine, pseudoisocytosine, 2-thiouracil, 2-thiothymidine, other naturally occurring nucleobase analogs, other non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties, biotin, fluorescein and dabcyl. In the most preferred embodiment, a PNA subunit consists of a naturally occurring or non-naturally occurring nucleobase attached to the aza nitrogen of the N-[2-(aminoethyl)]glycine backbone through a methylene carbonyl linkage.

f. As used herein, the terms "label" and "detectable moiety" shall be interchangeable and shall refer to moieties which can be attached to a non-nucleic acid probe, PNA probe, antibody or antibody fragment to thereby render the probe, antibody or antibody fragment detectable by an instrument or method.

g. As used herein, the term "chimera" or "chimeric oligomer" shall mean an oligomer comprising two or more linked subunits which are selected from different classes of subunits. For example, a PNA/DNA chimera would comprise at least two PNA subunits linked to at least one 2'-deoxyribonucleic acid subunit (For exemplary methods and compositions related to

PNA/DNA chimera preparation See: WO96/40709). Exemplary component subunits of the chimera are selected from the group consisting of PNA subunits, naturally occurring amino acid subunits, DNA subunits, RNA subunits and subunits of analogues or mimics of nucleic acids.

h. As used herein, the term "linked polymer" shall mean a polymer comprising two or more polymer segments which are linked by a linker. The polymer segments which are linked to form the linked polymer are selected from the group consisting of an oligodeoxynucleotide, an oligoribonucleotide, a peptide, a polyamide, a peptide nucleic acid (PNA) and a chimera.

2. Description

I. General:

PNA Synthesis:

Methods for the chemical assembly of PNAs are well known (See: United States Patent Nos. 5,539,082, 5,527,675, 5,623,049, 5,714,331, 5,736,336, 5,773,571, 5,786,461, 5,837,459, 5,891,625, 5,972,610 or 5,986,053, herein incorporated by reference). Chemicals and instrumentation for the support bound automated chemical assembly of peptide nucleic acids are now commercially available. Both labeled and unlabeled PNA oligomers are likewise available from commercial vendors of custom PNA oligomers. Chemical assembly of a PNA is analogous to solid phase peptide synthesis, wherein at each cycle of assembly the oligomer possesses a reactive alkyl amino terminus which is condensed with the next synthon to be added to the growing polymer. Because standard peptide chemistry is utilized, natural and non-natural amino acids are routinely incorporated into a PNA oligomer. Because a PNA is a polyamide, it has a C-terminus (carboxyl terminus) and an N-terminus (amino terminus). For the purposes of the design of a hybridization probe suitable for antiparallel binding to the target sequence (the preferred orientation), the N-terminus of the probing nucleobase sequence of the PNA probe is the equivalent of the 5'-hydroxyl terminus of an equivalent DNA or RNA oligonucleotide.

PNA Labeling:

Preferred non-limiting methods for labeling non-nucleic acid probes and PNAs are described in WO98/24933, WO99/22018, WO99/21881; copending and co-owned applications USSN 09/179,298, USSN 09/179,162, USSN 09/225,048 and USSN 09/275,848 (herein incorporated by reference), the priority documents listed as related applications, the examples section of this specification or are otherwise well known in the art of PNA synthesis.

Labels:

Non-limiting examples of detectable moieties (labels) suitable for labeling non-nucleic acid probes, PNAs or antibodies used in the practice of this invention would include a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound. Other suitable labeling reagents and preferred methods of attachment would be recognized by those of ordinary skill in the art of PNA, peptide or nucleic acid synthesis.

Preferred haptens include 5(6)-carboxyfluorescein, 2,4-dinitrophenyl, digoxigenin, and biotin.

Preferred fluorochromes (fluorophores) include 5(6)-carboxyfluorescein (Flu), 6-((7-amino-4-methylcoumarin-3-acetyl)amino)hexanoic acid (Cou), 5(and 6)-carboxy-X-rhodamine (Rox), Cyanine 2 (Cy2) Dye, Cyanine 3 (Cy3) Dye, Cyanine 3.5 (Cy3.5) Dye, Cyanine 5 (Cy5) Dye, Cyanine 5.5 (Cy5.5) Dye Cyanine 7 (Cy7) Dye, Cyanine 9 (Cy9) Dye (Cyanine dyes 2, 3, 3.5, 5 and 5.5 are available as NHS esters from Amersham, Arlington Heights, IL) or the Alexa dye series (Molecular Probes, Eugene, OR).

Preferred enzymes include polymerases (e.g. Taq polymerase, Klenow DNA polymerase, T7 DNA polymerase, Sequenase, DNA polymerase 1 and phi29 polymerase), alkaline phosphatase (AP), horseradish peroxidase (HRP) and most preferably, soy bean peroxidase (SBP).

Detectable and Independently Detectable Moieties/Multiplex Analysis:

In preferred embodiments of this invention, a multiplex hybridization assay is performed. In a multiplex assay, numerous conditions of interest are simultaneously examined. Multiplex analysis relies on the ability to sort sample components or the data associated therewith, during or after the assay is completed. In preferred embodiments of the invention, one or more distinct independently detectable moieties are used to label two or more different probes used in an assay. The ability to differentiate between and/or quantitate each of the independently detectable moieties provides the means to multiplex a hybridization assay because the data which correlates with the hybridization of each of the distinctly (independently) labeled probe to a particular target sequence can be correlated with the presence, absence or quantity of each of two or more chromosomes sought to be detected in the sample. Consequently, the multiplex assays of this invention may be used to simultaneously detect the presence, absence and/or number of two or more chromosomes in the same sample and in the same assay.

Spacer/Linker moieties:

Generally, spacers are used to minimize the adverse effects that bulky labeling reagents might have on hybridization properties of probes. Linkers typically induce flexibility and randomness into the probe or otherwise link two or more nucleobase sequences of a probe or component polymer. Preferred spacer/linker moieties for the nucleobase polymers of this invention consist of one or more aminoalkyl carboxylic acids (e.g. aminocaproic acid) the side chain of an amino acid (e.g. the side chain of lysine or ornithine) natural amino acids (e.g. glycine), aminooxyalkylacids (e.g. 8-amino-3,6-dioxaoctanoic acid), alkyl diacids (e.g. succinic acid), alkyloxy diacids (e.g. diglycolic acid) or alkyldiamines (e.g. 1,8-diamino-3,6-dioxaoctane). Spacer/linker moieties may also incidentally or intentionally be constructed to improve the water solubility of the probe (For example see: Gildea et al., *Tett. Lett. 39:* 7255-7258 (1998)). Preferably, a spacer/linker moiety comprises one or more linked compounds having the formula: -Y-$(O_m$-$(CW_2)_n)_o$-Z-. The group Y is selected from the group consisting of: a single bond, -$(CW_2)_p$-,-C(O)$(CW_2)_p$-, -C(S)$(CW_2)_p$- and -$S(O_2)(CW_2)_p$. The group Z has the formula NH, NR^2, S or O. Each W is independently H, R^2, -OR^2, F, Cl, Br or I; wherein, each R^2 is independently selected from the group consisting of: -CX_3, -CX_2CX_3, -$CX_2CX_2CX_3$, -$CX_2CX(CX_3)_2$, and-$C(CX_3)_3$. Each X is independently H, F, Cl, Br or I. Each m is independently 0 or 1. Each n, o and p are independently whole numbers from 0 to 10.

Hybridization Conditions/Stringency:

Those of ordinary skill in the art of nucleic acid hybridization will recognize that factors commonly used to impose or control stringency of hybridization include formamide concentration (or other chemical denaturant reagent), salt concentration (i.e., ionic strength), hybridization temperature, detergent concentration, pH and the presence or absence of chaotropes. Optimal stringency for a probe/target combination is often found by the well known technique of fixing several of the aforementioned stringency factors and then determining the effect of varying a single stringency factor. The same stringency factors can be modulated to thereby control the stringency of hybridization of a non-nucleic acid probe or PNA probe to a nucleic acid, except that the hybridization of a PNA is fairly independent of ionic strength. Optimal stringency for an assay may be experimentally determined by examination of each stringency factor until the desired degree of discrimination is achieved.

Suitable Hybridization Conditions:

Generally, the more closely related the background causing nucleic acid contaminates are to the target sequence, the more carefully stringency must be controlled. Blocking probes may also be used as a means to improve discrimination beyond the limits possible by mere

optimization of stringency factors. Suitable hybridization conditions will thus comprise conditions under which the desired degree of discrimination is achieved such that an assay generates an accurate (within the tolerance desired for the assay) and reproducible result. Aided by no more than routine experimentation and the disclosure provided herein, those of skill in the art will easily be able to determine suitable hybridization conditions for performing assays utilizing the methods and compositions described herein. Suitable *in-situ* hybridization conditions are those conditions suitable for performing an *in-situ* hybridization procedure. Thus, suitable *in-situ* hybridization conditions will become apparent to those of skill in the art by using the disclosure provided herein; with or without additional routine experimentation.

Blocking Probes:

Blocking probes are nucleic acid or non-nucleic acid probes which can be used to suppress the binding of the probing nucleobase sequence of the probing polymer to a non-target sequence. Preferred blocking probes are PNA probes (See: Coull et al., WIPO publication No. WO98/24933). Typically blocking probes are closely related to the probing nucleobase sequence and preferably they comprise a point mutation of the probing segment. It is believed that blocking probes operate by hybridization to the non-target sequence to thereby form a more thermodynamically stable complex than is formed by hybridization between the probing nucleobase sequence and the non-target sequence. Formation of the more stable and preferred complex blocks formation of the less stable non-preferred complex between the probing nucleobase sequence and the non-target sequence. Thus, blocking probes can be used with the methods, kits and compositions of this invention to suppress the binding of the nucleic acid or non-nucleic acid probe to a non-target sequence which might be present and interfere with the performance of the assay. Blocking probes are particularly advantageous in single point mutation discrimination.

Probing Nucleobase Sequence:

The probing nucleobase sequence of a non-nucleic acid probe of this invention is the sequence recognition portion of the construct. Therefore, the probing nucleobase sequence is designed to hybridize to at least a portion of the target sequence. Preferably, the probing nucleobase sequence hybridizes to the entire target sequence. Detection of probe hybridization can be correlated with the presence, absence or number of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in a sample. Consequently, with due consideration of the requirements of a non-nucleic acid probe for the assay format chosen and the human chromosome sought to be detected, the length and nucleobase content of the probing nucleobase sequence of the non-

nucleic acid probe will generally be chosen such that a stable complex is formed with the target sequence of the chromosome of interest, under suitable hybridization conditions or suitable *in-situ* hybridization conditions.

The non-nucleic acid probes of this invention are relatively short as compared with the nucleic acid probes (0.1 to 5 kb or larger) which have been typically been used in ISH or FISH assays for the detection of chromosomes. The non-nucleic acid probe suitable for the practice of this invention will preferably have a length of 10-30 subunits wherein the exact probing nucleobase sequence is at least ninety percent homologous to the nucleobase sequences listed in Table 1, or their complements. Specifically, the probing nucleobase sequence of the non-nucleic acid probes of this invention will preferably be in the range of 15-25 subunits in length and most preferably 17-23 subunits in length. Non-nucleic acid probes containing shorter probing nucleobase sequences shall typically be designed by truncating the probing nucleobase sequences listed in Table 1. The most preferred probing nucleobase sequences are listed in Table 1. Non-nucleic acid probes comprising these particular probing nucleobase sequences have been observed by Applicant to be specific for the human chromosomes sought to be detected. By specific we mean that the Applicant, using a standard protocol and several different cell lines, has achieved a very high degree of hybridization specificity such that little or no detectable cross hybridization to other human chromosomes has been observed. This is most remarkable given that identical stringency conditions have been applied in all assays performed without regard to the substantial sequence and length differnces of the non-nucleic acid probes identified in Table 2.

The significant cross reaction between the nucleic acid probes can potentially lead to errors in automated analysis since these could erroneously be interpreted as aneuploidy or polyploidy karyotypes. With regard to multiplex analysis, the potential for errors will also increase since small amounts of cross hybridization will be cumulative. Thus, a large number of cross reactions to a single non-target chromosome can lead to a very significant non-specific signal in the assay which cannot be ignored, filtered or subtracted out as background.

This invention contemplates that variations in the probing nucleobase sequences listed in Table 1 shall provide non-nucleic acid probes which are suitable for the specific detection of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18. Common variations include, truncations, deletions, insertions and frame shifts. Variation of the probing nucleobase sequences within the parameters described herein are considered to be an embodiment of this invention.

The probing nucleobase sequence of a non-nucleic acid probe will preferably be exactly complementary to the target sequence. Alternatively, a substantially complementary probing nucleobase sequence might be used since it has been demonstrated that greater sequence discrimination can be obtained when utilizing probes wherein there exists one or more point mutations (base mismatch) between the probe and the target sequence (See: Guo et al., *Nature Biotechnology* 15:331-335 (1997).

The non-nucleic acid probes of this invention are further characterized in that the backbone of the probing nucleobase sequence of the probe is neutral or positively charged under suitable hybridization conditions or suitable *in-situ* hybridization conditions. Without intending to be bound to this hypothesis, it is believed that the neutral or positively charged backbone provides the probe with better access to the double stranded nucleic acid target sequence of the chromosome.

Probe Complexes:

In still another embodiment, two probes are designed to hybridize to the target sequence sought to be detected to thereby generate a detectable signal whereby the probing nucleobase sequence of each probe comprises the complement to half or approximately half of the complete target sequence of the chromosome sought to be detected in the assay. As a non-limiting example, the probing nucleobase sequences of the two probes might be designed using the assay as described in European Patent Application 849,363, entitled "Method of identifying a nucleic acid using triple helix formation of adjacently annealed probes" by H. Orum et al. (See: EPA 849,363). Using this methodology, the probes which hybridize to the target sequence need not be labeled since it is the probe complex formed by the annealing of the adjacent probes which is detected. Similar compositions comprised solely of PNA probes have been described in copending and commonly owned application USSN 09/302,238, herein incorporated by reference.

II. Preferred Embodiments of the Invention:

a. Non-Nucleic Acid Probes:

In one embodiment, this invention is directed to non-nucleic acid probes. The non-nucleic acid probes of this invention are suitable for detecting, identifying or quantitating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in a sample or in the individual cells of a sample. General characteristics and attributes (e.g. length, labels, and linkers etc.) of the non-nucleic acid probes suitable for the detection, identification or quantitation of human

chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 have been previously described herein (See the discussion under the section entitled: "General"). The preferred probing nucleobase sequences of non-nucleic acid probes of this invention are listed in Table 1.

TABLE 1

Target Human Chromosome	Probing Nucleobase Sequence	Seq. ID No.
X	CTT-CAA-AGA-GGT-CCA-CGA	1
X	AGG-GTT-CAA-CTG-TGT-GAC	2
X	GAA-ACT-TCT-GAG-TGA-TGA	3
X	CAG-TCA-TCG-CAG-AAA-ACT	4
X	AGA-TTT-CAC-TGG-AAA-CGG	5
X	GTT-ATG-GGA-AGG-TGA-TCC	6
X	TCG-AGC-CGC-AGA-GTT-TAA	7
X	CTA-TTT-AGC-GGG-CTT-GGA	8
X	TAC-AAG-GGT-GTT-GCA-AAC	9
Y	CCA-TAT-GCA-GTT-ATA-AGT-AGG	10
Y	TAT-TGT-ACC-AAG-CAG-AGT-ACC	11
Y	GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA	12
Y	GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT	13
Y	TCA-CAT-AAT-AGA-CAA-CAT-AC	14
Y	CAG-AAG-AGA-TTG-AAC-CTT	15
Y	GGC-ATA-GCA-CAT-AAC-ATG	16
1	AAT-CGT-CAT-CGA-ATG-AAT	17
1	CAT-TGA-ACA-GAA-TTG-AAT	18
2	GTT-TTC-AGG-GGA-AGA-TAT	19
2	TGT-GCG-CCC-TCA-ACT-AAC	20
2	GAA-GCT-TCA-TTG-GGA-TGT	21
2	CCA-ATA-AAA-GCT-ACA-TAG-A	22
2	GAA-AAA-GTT-TCT-GAC-ATT-GC	23
2	TAG-TTG-AAG-GGC-ACA-TCA	24
2	CAC-AAA-TAA-GAT-TCT-AAG-AAT	25
2	TCA-AAA-GAA-TGC-TTC-AAC-AC	26
3	ATA-ATT-AGA-CCG-GAA-TCA-T	27
3	GCT-GTT-TTC-TAA-AGG-AAA-G	28
3	AAG-ACT-TCA-AAG-AGG-TCC	29
3	TTT-GTC-AAG-AAT-TAT-AAG-AAG	30
3	CAA-GAT-TGC-TTT-TAA-TGG	31
3	TGT-GTA-TCA-ACT-CAC-GGA	32
3	CCT-CAC-AAA-GTA-GAA-ACT	33
3	GAA-AAA-GCA-GTT-ACT-GAG	34
3	TAA-TAA-TTA-GAC-GGA-ATC-AT	35

3	TTA-CAG-GGC-ATT-GAA-GCC	36
3	CAG-TTA-TGA-AGC-AGT-CTC	37
3	CAC-ACC-AGA-AAA-AGC-AGT	38
3	AAG-GGT-AAA-CAC-TGT-GAG	39
3	AGA-CAA-CGA-AAT-ATC-TTC-ATG	40
3	CTA-GCA-GTA-TGA-GGT-CAA	41
3	GCA-GAC-TTC-AGA-AAC-AGA	42
3	GGC-CTC-AAA-GAC-GTT-TAA	43
3	GTG-AAA-GTT-CCA-AGT-GAA	44
3	GAG-TGC-TTT-GAA-GCC-TAC	45
3	GAA-ACA-GCA-GAG-TTG-AAA	46
3	TGC-AGA-GAT-CAC-AAC-GTG	47
3	ACA-AAG-AAT-CAT-TCG-CAG	48
3	AGT-GTT-AGA-AAA-CTG-CTC	49
6	CTG-TTC-AGA-GTA-ACA-TGA	50
6	CCG-CTT-GGA-AAT-ACT-ACA	51
6	GAA-ATG-GAA-ATA-TCT-CCC-C	52
6	TCT-AGG-AGG-TCC-AAT-TAT	53
6	GAA-TTC-CCA-AGT-GGA-TAT	54
6	CTG-TAG-GTT-TAG-ATG-AAG	55
6	AAG-GAG-TGT-TTC-CCA-ACT	56
6	GGC-TTC-AAG-GCG-CTC-TAA	57
6	GCA-GAG-ACT-TCA-AAG-TGC	58
6	CAC-ACA-CAC-GGT-GGA-CCA	59
6	CAA-AGG-GAA-TGT-TCC-ATT	60
6	CAC-ATA-GCA-GTG-TTT-GAG	61
6	CTC-AAG-GCG-GTC-CAA-TTA	62
6	GAG-TCG-AAA-TGC-ACA-CAT	63
6	TAC-CAA-GAG-GAA-TGT-TGC	64
8	ACG-GGA-TGC-AAT-ATA-AAA	65
8	TGA-AGA-TTC-TGC-ATA-CGG	66
8	AAG-GTT-TGT-ACT-GAC-AGA	67
8	CTG-AAC-TAT-GGT-GAA-AAA	68
8	ACT-AAC-TGT-GCT-GAA-CAT	69
8	CCC-ATG-AAT-GCG-AGA-TAG	70
10	AAC-TGA-ACG-CAC-AGA-TGA	71
10	GGC-TAA-TCT-TTG-AAA-TTG-AAA	72
10	AGG-TGG-ATA-ATT-GGC-CCT	73
10	TGA-AGT-CCA-AAA-AAG-CAC	74
10	CTT-AGA-CAT-GGA-AAT-ATC	75
10	AAG-GGG-TCT-AAC-TAA-TCA	76
10	GTA-GTT-GTT-GAG-AAT-GAT	77
11	AAC-TTC-CCA-GAA-CTA-CAC	78
11	ATT-CTT-GAA-ATG-GAA-CAC	79

11	CTG-TGA-TTG-CTG-ATT-TGG	80
11	GTC-ATC-ACA-GGA-AAC-ATT	81
11	GAA-ATT-TCC-TGT-TGA-CAG-A	82
11	GTT-TGA-AAG-CTG-AAC-TAT-G	83
12	TCC-TGT-AAT-GTT-CGA-CAG	84
12	TCA-TAG-AAC-GCT-AGA-AAG	85
12	ACC-TTT-CTT-TTG-ATG-AAG-GA	86
12	CAA-ATA-TCA-CAA-AAA-GAG-GG	87
12	GAG-TTG-AAT-AGA-GGC-AAC	88
12	GGC-CAA-ATG-TAG-AAA-AGG	89
12	GCG-TTC-AAC-TCA-AGG-TGT	90
12	TGT-CCT-TTA-GAC-AGA-GCA	91
12	TGA-GAC-CAA-ATG-TAC-AAA-AG	92
12	GAA-TAC-TGA-GTA-AGT-TCT-TTG	93
12	AAC-TGC-ACA-AAT-AGG-GTG	94
12	TGG-AGA-CAC-TGT-GTT-TGT	95
12	CCA-GTT-GGA-GAT-TTC-AAT	96
16	GAA-GCC-TGC-CAG-TGG-ATA	97
16	TAC-AGC-ATT-CTG-GAA-ACC	98
16	CCA-GAC-ACT-GCG-TAG-TGA	99
16	ATA-TAA-TGC-TAG-AGG-GAG	100
16	AAA-AAC-AAG-ACA-AAC-TCG	101
17	ATT-TCA-GCT-GAC-TAA-ACA	102
17	AAC-GAA-TTA-TGG-TCA-CAT	103
17	GGT-GAC-GAC-TGA-GTT-TAA	104
17	TTT-GGA-CCA-CTC-TGT-GGC	105
17	AAC-GGG-ATA-ACT-GCA-CCT	106
17	TTT-GTG-GTT-TGT-GGT-GGA	107
17	AGG-GAA-TAG-CTT-CAT-AGA	108
17	ATC-ACG-AAG-AAG-GTT-CTG	109
17	CCG-AAG-ATG-TCT-TTG-GAA	110
17	AAA-GAG-GTC-TAC-ATG-TCC	111
18	TTC-CCG-TAA-CAA-CTA-TGC	112
18	TCC-CGT-AAC-AAC-TAG-GCA	113
18	AAA-AGG-AGT-GAT-CCA-ACC	114
18	TCC-CTT-TGG-TAG-AGC-AGG	115
18	ATT-TGA-GAT-GTG-TGT-ACT-CA	116
18	GCA-CTT-ACC-GGC-CTA-AG	117
18	CTC-AGA-AAC-TTA-CTC-GTG	118

Note: Apart from the functional examples described herein which have been performed to screen potential probe sequences and thereby confirm their practical specificity in an assay, the complementary target sequence to which the probing nucleobase sequences in Table 1 hybridize

were examined using sequence alignment analysis of information currently available in Genbank. It is noteworthy that in the functional assay many of the sequences originally chosen did not prove to be highly specific despite alignment analysis indications that they should be specific to the chromosome sought to be detected.

The probing nucleobase sequences listed in Table 1 are complementary to target sequences which are highly repetitive within the chromosome sought to be detected. Since the chromosomal DNA is double stranded, the complement to the probing nucleobase sequences listed in Table 1 will also provide a probe suitable for hybridization to the complementary strand. Typically, the target sequence is repeated between 100 to 5000 times within the chromosome. Consequently, although each probe is typically labeled with a single detectable moiety, signal generated from the fluorophores (the preferred detectable moiety) concentrated on the chromosome sought to be detected with the non-nucleic acid probes of this invention is easily visible to the eye using a conventional fluorescence microscope.

Applicant has estimated that approximately 200 fluorophores concentrated in the chromosome are necessary to visualize a detectable signal using conventional microscopy. Consequently, it is preferable to choose non-nucleic acid probes directed to a target sequence which is repeated at least 200 times in the chromosome. Alternatively, non-nucleic acid probes can be chosen which have a target sequence which is repeated fewer than 200 times provided more than one probe to a particular chromosome is used in the assay. For example, two or more non-nucleic acid probes could be used provided that each target sequence was repeated one hundred times within the chromosome sought to be detected. Alternatively, multiple labels could be attached to each probe to thereby increase detectable signal by a factor commensurate with the number of attached labels and the number of available targets to thereby achieve the level of fluorescence intensity required to achieve a detectable signal. It is also anticipated that as more intense fluorophores are developed or more sensitive methods of detection become available, the number of target sequence repeats or number of probes per cocktail necessary to achieve a satisfactory level of signal in a assay for a particular chromosome will drop.

The non-nucleic acid probes of this invention may comprise only a probing nucleobase sequence or may comprise additional moieties. Non-limiting examples of additional moieties include detectable moieties (labels), linkers, spacers, natural or non-natural amino acids, or other subunits of PNA, DNA or RNA. Additional moieties may be functional or non-functional in an assay. Generally however, additional moieties will be selected to be functional within the

design of the assay in which the non-nucleic acid probe is to be used. The preferred non-nucleic acid probes of this invention are labeled with one or more detectable moieties. In a more preferred embodiment, one or more probes are labeled with two or more independently detectable moieties. Preferred independently detectable moieties are independently detectable fluorophores. Preferred probes of this invention will also comprise solubility enhancer moieties such as those described in: Gildea et al., *Tett. Lett. 39:* 7255-7258 (1998) or copending and co-owned patent application USSN 09/225,048, herein incorporated by reference. The solubility enhancers are typically used to enable the synthesis and purification of the PNA which otherwise may be insoluble or tend to self aggregate. The solubility enhancers are particularly useful in the synthesis and purification of the numerous labeled purine rich probes listed in Table 2.

In a most preferred embodiment of this invention, independently detectable moieties are used to label each of at least two different non-nucleic acid probes, whereby at least one probe is suitable for detecting one of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 and at least one other probe is suitable for detecting another of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18, such that the independently detectable moieties can be used to independently detect, identify or quantitate each of at least two different chromosome types in the same assay. In certain preferred embodiments, one or more of the probes may comprise two or more independently detectable moieties wherein the combination of the two or more labels is unique in the assay and can be used to detect the presence or amount of the chromosome of interest in the sample. More specifically, the presence or amount of the unique combination of labels in the sample is indicative of the presence or amount of the probe/target sequence hybrid characteristic for the chromosome sought to be detected.

In preferred embodiments, the probes of this invention are used in *in-situ* hybridization (ISH) and fluorescence *in-situ* hybridization (FISH) assays. Excess probe used in a ISH or FISH assay typically must be removed so that the detectable moiety of specifically bound probes can be detected above the background signal which results from still present but unhybridized probe. Generally, the excess probe is washed away after the sample has been incubated with probe for a period of time. However, use of dark probes are a preferred embodiment of this invention, since there is no requirement that excess dark probe be completely removed (washed away) from the sample since the unhybridized probe generates little or no detectable background in the assay.

As used herein, a "dark probe" shall be a probe which hybridizes to a target sequence to thereby cause a detectable change in at least one physical property of at least one attached label in a manner which can be used to detect, identify or quantitate the presence of an organism of interest in a sample of interest. Non-limiting examples of "dark probes" include nucleic acid Molecular Beacons (See: WO97/39008 and US 5,925,517), PNA Molecular Beacons (See: WO99/21881 and USSN 08/958,532 (abandoned) and copending and commonly owned USSN 09/179,298, both incorporated herein by reference), Linear Beacons (See: WO99/22018 and copending and commonly owned USSN 09/179,162, herein incorporated by reference) and probes comprising a reporter which intercalates upon hybridization to thereby produce fluorescence. (See: WO97/45539). Thus, changes in signal in the assay utilizing a "dark probe" can be directly or indirectly correlated with hybridization of the probing nucleobase sequence to the target sequence of the chromosome of interest.

Unlabeled Non-Nucleic Acid Probes:

The probes of this invention need not be labeled with a detectable moiety to be operable within this invention. When using the probes of this invention it is possible to detect the probe/target sequence complex formed by hybridization of the probing nucleobase sequence of the probe to the target sequence. For example, a PNA/nucleic acid complex formed by the hybridization of a PNA probing nucleobase sequence to the target sequence could be detected using an antibody which specifically interacts with the complex under antibody binding conditions. Suitable antibodies to PNA/nucleic acid complexes as well as methods for their preparation and use are described in WIPO Patent Application WO95/17430 and US 5,612,458, herein incorporated by reference. Antibodies to complexes formed with non-nucleic acid probes other than PNA can likewise be prepared using methods similar to those described in WIPO Patent Application WO95/17430 and US 5,612,458.

The antibody/PNA/nucleic acid complex formed by interaction of the α-PNA/nucleic acid antibody with the PNA/nucleic acid complex can be detected by several methods. For example, the α-PNA/nucleic acid antibody could be labeled with a detectable moiety. Suitable detectable moieties have been previously described herein. Thus, the presence, absence or quantity of the detectable moiety is correlated with the presence, absence or quantity of the antibody/PNA/nucleic acid complex and the chromosome to be identified by the probing nucleobase sequence of the PNA probe. Alternatively, the antibody/PNA/nucleic acid complex is detected using a secondary antibody which is labeled with a detectable moiety. Typically the secondary antibody specifically binds to the α-PNA/nucleic acid antibody under antibody

binding conditions. Thus, the presence, absence or quantity of the detectable moiety is correlated with the presence, absence or quantity of the antibody/antibody/PNA/nucleic acid complex and the chromosome to be identified by the probing nucleobase sequence of the probe. As used herein, the term antibody shall include antibody fragments which specifically bind to other antibodies or other antibody fragments.

Immobilization of Probes To A Surface:

One or more of the non-nucleic acid probes of this invention may optionally be immobilized to a surface for the detection identification or quantitation of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18. Non-nucleic acid probes can be immobilized to the surface using the well known process of UV-crosslinking. More preferably, the non-nucleic acid probe is synthesized on the surface in a manner suitable for deprotection but not cleavage from the synthesis support (See: Weiler, J. et al, Hybridization based DNA screening on peptide nucleic acid (PNA) oligomer arrays., Nucl. Acids Res., 25: 2792-2799 (July, 1997)). In still another embodiment, one or more non-nucleic acid probes are covalently linked to a surface by the reaction of a suitable functional group on the probe with a functional group of the surface (See: Lester, A. et al, "PNA Array Technology": Presented at Biochip Technologies Conference in Annapolis (October, 1997)). This method is most preferred since the non-nucleic acid probes on the surface will typically be highly purified and attached using a defined chemistry, thereby minimizing or eliminating non-specific interactions.

Methods for the chemical attachment of probes to surfaces generally involve the reaction of a nucleophilic group, (e.g. an amine or thiol) of the probe to be immobilized, with an electrophilic group on the support to be modified. Alternatively, the nucleophile can be present on the support and the electrophile (e.g. activated carboxylic acid) present on the probe. Because native PNA possesses an amino terminus, a PNA will not necessarily require modification to thereby immobilize it to a surface (See: Lester et al., Poster entitled "PNA Array Technology").

Conditions suitable for the immobilization of a non-nucleic acid probe to a surface will generally be similar to those conditions suitable for the labeling of the polymer. The immobilization reaction is essentially the equivalent of labeling whereby the label is substituted with the surface to which the polymer is to be linked.

Numerous types of surfaces derivatized with amino groups, carboxylic acid groups, isocyantes, isothiocyanates and malimide groups are commercially available. Non-limiting

examples of suitable surfaces include membranes, glass, controlled pore glass, polystyrene particles (beads), silica and gold nanoparticles.

Arrays of PNA Probes or Probe Sets:

Arrays are surfaces to which two or more probes have been immobilized each at a specified position. This invention is also directed to immobilized probes having probing nucleobase sequences judiciously chosen to interrogate (often using a capture assay) a sample to thereby detect the presence, absence or number of human chromosomes. Because the location and composition of each immobilized probe is known, arrays are generally useful for the simultaneously detection, identification or quantitation of two or more target sequences which may be present in the sample. Moreover, arrays of non-nucleic acid or PNA probes may be regenerated by stripping the hybridized nucleic acid after each assay, thereby providing a means to repetitively analyze numerous samples using the same array. Thus, arrays of non-nucleic acid or PNA probes may be useful for repetitive screening of samples for one or more chromosomes of interest. The arrays of this invention comprise at least one non-nucleic acid probe (as described herein) suitable for the detection, identification or quantitation of human chromosomes. Preferred probing nucleobase sequences for the immobilized non-nucleic acid probes are listed in Table 1.

Advantages Associated With Non-Nucleic Acid Probes:

Unlike oligonucleotide probes, non-nucleic acid probes lack a negative charge on the backbone of the nulceobase containing subunits and therefore they efficiently interact with the target sequence of the nucleic acid since there are no electrostatic forces which repel each other when the hybrid is formed. This allows for optimization of stringency conditions wherein a high degree of specificity of signal is achieved.

The non-nucleic acid probes of this invention also differ from the nucleic acid probes typically chosen for chromosome analysis since they are purified synthetic molecules which are highly defined and well characterized. Consequently, the non-nucleic acid probes or the mixtures of non-nucleic acid probes can be more easily reproduced than are the nucleic acid probes with are typically derived by enzymatic manipulation of nucleic acid starting materials. Thus, the non-nucleic acid probes or the mixtures of non-nucleic acid probes of this invention should be more homogenous from lot to lot thereby reducing the lot to lot performance variability often associated with nucleic acid probes.

b. Probe Sets:

In another embodiment, this invention is directed to a probe set suitable for detecting, identifying or quantitating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 present in a sample or in the cells of a sample. General and preferred characteristics of non-nucleic acid probes suitable for preparing a probe set useful for the detection, identification or quantitation of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 have been previously described herein. Preferred probing nucleobase sequences are listed in Table 1. The grouping of non-nucleic acid probes within sets characterized for specific detection of one, two or more of the human chromosomes (e.g. X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18) is contemplated as a preferred embodiment of this invention. In preferred embodiments, one or more probe sets identified herein are combined with other probes to generate a probe set suitable for the detection, identification and/or enumeration of all human chromosomes in the same assay.

Probe sets of this invention shall comprise at least one non-nucleic acid probe but need not comprise only non-nucleic acid probes. For example, probe sets of this invention may comprise mixtures of non-nucleic acid probes and nucleic acid probes, provided however that a set comprises at least one non-nucleic acid probe as described herein. In preferred embodiments, some of the probes of the set are blocking probes composed of unlabeled PNA and/or nucleic acid oligomers.

Table 1 lists many alternative probing nucleobase sequences suitable for the detection, identification and/or quantitation of the identified human chromosomes of interest. Since alternative probing nucleobase sequences exist for the detection of any of the chromosomes, it is preferable to use a probe set containing two or more non-nucleic acid probes for the detection, identification and/or quantitation of a particular chromosome to thereby increase the detectable signal in the assay. In a preferred embodiment, all the probes of a set which are used to detect, identify and/or quantitate a particular chromosome will be labeled with the same independently detectable moiety or moieties and all probes of a set which are used to detect, identify and/or quantitate a different chromosome in the same sample will be labeled with one or more different independently detectable moieties to thereby enable the independent detection of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in the same sample and in the same assay (a multiplex assay). One exemplary probe set would therefore comprise probes suitable for the detection, identification and/or quantitation of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18 which might be present in a sample. For example, a suitable probe set might therefore contain at least one non-nucleic acid probe suitable for detecting each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18 but more preferably, the

preferred probe set would contain non-nucleic acid probes such that most or all of the probing nucleobase sequences listed in Table 1 are represented.

Consequently, an exemplary probe set might therefore comprise at least one non-nucleic acid probe suitable for detecting the human X chromosome, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1) ; AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9). The set would further comprise at least one non-nucleic acid probe suitable for detecting the human Y chromosome, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 1, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17) and CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 2, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25) and TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome

3, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48) and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 6, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63) and TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 8, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-

GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 10, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76) and GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 11, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 12, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 16, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100) and AAA-AAC-AAG-ACA-AAC-TCG (Seq.

ID No. 101). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 17, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110) and AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111). The set would further comprise at least one non-nucleic acid probe suitable for detecting human chromosome 18, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118).

In a preferred embodiment, probes of the set which are specific for detecting each particular chromosome would be independently detectable from probes for detecting the other chromosomes. This would enable the independent detection, identification and quantitation of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in the same sample and in the same assay. Most preferably, the probes of the set will be labeled with one or more independently detectable fluorophores to thereby enable correlation of a particular fluorophore, or set of fluorophores, with the presence of a particular chromosome.

A second exemplary probe set might comprise those non-nucleic acid probes suitable for the detection of human chromosome X. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome X, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq.

ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9).

A third exemplary probe might comprise those non-nucleic acid probes suitable for the detection of human chromosome Y. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human Y chromosome, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16).

A fourth exemplary probe set might comprise those non-nucleic acid probes suitable for the detection of human chromosome 1. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 1, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17) and CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18).

A fifth exemplary probe set might comprise those probes suitable for the detection of human chromosome 2. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 2, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25) and TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26).

A sixth exemplary probe set might comprise those probes suitable for the detection of human chromosome 3. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 3, wherein at least one

probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48) and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49).

A seventh exemplary probe might comprise those probes suitable for the detection of human chromosome 6. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 6, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63) and TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64).

An eighth exemplary probe might comprise those probes suitable for the detection of human chromosome 8. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 8, wherein at least one

probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70).

A ninth exemplary probe set might comprise those non-nucleic acid probes suitable for the detection of human chromosome 10. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 10, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76) and GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77).

A tenth exemplary probe set might comprise those non-nucleic acid probes suitable for the detection of human chromosome 11. A suitable probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 11, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83).

An eleventh exemplary probe set might comprise those non-nucleic acid probes suitable for the detection of human chromosome 12. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 12, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-

GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96).

A twelfth exemplary probe set might comprise those probes suitable for the detection of human chromosome 16. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 16, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100) and AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101).

A thirteenth exemplary probe might comprise those probes suitable for the detection of human chromosome 17. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 17, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110) and AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111).

Still a fourteenth exemplary probe set might comprise those non-nucleic acid probes suitable for the detection of human chromosome 18. A suitable exemplary probe set might therefore comprise at least two non-nucleic acid probes suitable for detecting the human chromosome 18, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or there complements, which are selected from the group consisting of: TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115);

ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118).

Multiplex Probe Sets For PNA-FISH Assays:

Because the individual non-nucleic acid probes of this invention can each be labeled with one or more independently detectable moieties, it is possible to design probe sets wherein each non-nucleic acid probe of the set are independently detectable. Fluorophores which have sufficiently different excitation and emission spectra are often used as independently detectable moieties. A non-limiting example of exemplary independently detectable fluorophores can be found in the section of this specification entitled "Labels". Thus, an assay utilizing a probe set comprising two or more non-nucleic acid probes, each labeled with one or more independently detectable moieties, could be used to independently detect, identify or quantitate the number of the human chromosome X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in the same assay. Consequently, the non-nucleic acid probes, probe sets, methods and kits of this invention are particularly useful for the rapid, sensitive, reliable and versatile multiplex analysis of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18 in a single sample and same assay. By versatile we mean that the method is generally applicable despite substantial variability in the length and nucleobase content of the probes used in the assay. In most preferred embodiments, the set of non-nucleic acid probes are suitable for the detection, identification and/or quantitation of all human chromosomes in the same sample and in the same assay (e.g. a multiplex assay).

c. Methods:

In another embodiment, this invention is directed to a method suitable for detecting, identifying and/or quantitating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample or in the individual cells of a sample. The general and preferred characteristics of non-nucleic acid probes and probe sets suitable for the detection, identification and/or quantitation of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 have been previously described herein. Preferred probing nucleobase sequences are listed in Table 1. Preferably, the method is used for the simultaneous detection of all human chromosomes in the same assay and most preferably the assay is an automated multiplex PNA-ISH or PNA-FISH assay. Most preferably, the assay is automated and performed using either a slide scanner based analysis system, microscope and camera (e.g. CCD camera) or a flow cytometer.

According to the method, the sample is contacted with one or more non-nucleic acid probes having a probing nucleobase sequence which is specific for one or more of human

chromosomes selected from the group consisting of X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18. The one or more chromosomes are then detected, identified and/or quantitated. Detection, identification and/or quantitation is made possible by monitoring the hybridization under suitable hybridization conditions or suitable *in-situ* hybridization conditions, of the probing nucleobase sequence of non-nucleic acid probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes sought to be detected in the sample. Typically, this correlation is made possible by direct or indirect detection of the probe/target sequence hybrid. This method is particularly advantageous for scoring the number of human chromosomes per cell. The number of chromosomes per cell is particularly useful in karyotype analysis.

In preferred embodiments, the method for detecting, identifying or quantitating human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample comprise contacting the sample with one or more non-nucleic acid probes, wherein at least one probe of the set has a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the probing nucleobase sequences, or there complements, which are selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-

AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID

No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116) ; GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118).

Exemplary probe sets specific to each chromosome and preferred probing nucleobase sequences suitable for the preparation of chromosome specific non-nucleic acid probes have previously been described herein. In a preferred embodiment, the method can be multiplexed to provide specific detection, identification and/or quantitation of each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a single assay provided that the non-nucleic acid probes for a particular chromosome (X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18) are independently detectable. In a preferred embodiment, non-nucleic acid probes used to detect each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 are each labeled with one or more independently detectable fluorophores to thereby enable correlation of signal from a particular fluorophore, or set of fluorophores, with the presence, absence and/or quantity of one of either chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18. The grouping of non-nucleic acid probes within probe sets characterized for detecting, identification and/or quantitation or one, two or all of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18 in the same assay is contemplated as a preferred embodiment of this invention. Most preferably, the set of non-nucleic acid probes is designed to detect, identify and/or quantitate most or all the human chromosomes from one or more samples in a single assay (e.g. a multiplex assay).

Exemplary Assay Formats:

The probes, probe sets, methods and kits of this invention are suitable for the detection, identification and/or quantitation of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17

and/or 18. In preferred embodiments, *in-situ* hybridization is used as the assay format for detecting identifying and/or quantitating chromosomes in a sample. Most preferably, fluorescence *in-situ* hybridization (FISH or PNA-FISH) is the assay format. Exemplary methods for performing PNA-ISH can be found in: Thisted et al. Cell Vision, 3:358-363 (1996), WIPO Patent Application WO97/18325, herein incorporated by reference or WIPO Patent Application WO97/14026, herein incorporated by reference.

Methods used to experimentally test the non-nucleic acid probes of this invention in PNA-FISH assays can be found in Examples 9 and 10 of this specification. Figures 1-16 demonstrate that labeled non-nucleic acid probes comprising the probing nucleobase sequences listed in Table 1 (actual PNA probe compositions are listed in Table 2) are specific for the human chromosome sought to be detected. Furthermore, the speed and reproducibility of the protocol and the unambiguous results achieved using the non-nucleic acid probes of this invention is believed to be superior to those typically achieved with nucleic acid probes. Using previously fixed cells, the experimental conditions used in the Examples will yield results within approximately 1-2 hours. Furthermore, the assays performed were found to be sensitive, reliable, reproducible and generally applicable without regard to the substantial variability in sequence length or composition or label of the numerous probes tested (118 probing nucleobase sequences made and tested with a variability in length of 17 to 23 nucleobases including the analysis of three different labeling reagents (Cy5, Flu and Rox). This is a very surprising result given that the same assay conditions were found to be suitable for specific detection of different chromosomes using no less than 118 non-nucleic acid probes of such dramatically different composition.

Samples which have been treated with the non-nucleic acid probes or probe sets contained in the kits of this invention can be detected by several exemplary methods. Samples of cells or tissues can be fixed on slides and then visualized with a microscope or laser scanning device. Alternatively, the samples or cells can be fixed and then analyzed in a flow cytometer (See for example: Lansdorp et al.; WIPO Patent Application; WO97/14026). Slide scanners and flow cytometers are particularly useful for rapidly quantitating the number of total chromosomes or individual types of chromosomes (e.g. 1, 2, X, Y etc.) present in a single sample of interest.

d. Kits:

In yet another embodiment, this invention is directed to kits suitable for performing an assay which detects the presence, absence and/or number of human chromosomes X, Y, 1, 2, 3,

6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample or in the individual cells of a sample. The general and preferred characteristics of non-nucleic acid probes suitable for the detection, identification or quantitation of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 have been previously described herein. Preferred probing nucleobase sequences are listed in Table 1. Furthermore, methods suitable for using the non-nucleic acid probes or probes sets of a kit to detect, identify and/or quantitate human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 have been previously described herein. Preferably, the kits are used in an assay suitable for simultaneous detection, identification and/or quantitation of all human chromosomes and most preferably the assay is an automated PNA-FISH assay. Most preferably, the assay is automated and performed using either a slide scanner based analysis system, microscope and CCD camera or a flow cytometer.

The kits of this invention comprise one or more non-nucleic acid probes and optionally one or more other reagents or compositions which are selected to perform an assay or otherwise simplify the performance of an assay used to detect, identify and/or quantitate human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in a sample. In kits which contain sets of non-nucleic acid probes wherein each of at least two probes of the set are used to distinctly detect, identify and/or quantitate each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 in the same sample and in the same assay, each of the probes of the set are preferably labeled with one or more independently detectable moieties. In a preferred embodiment, non-nucleic acid probes of a kit which are used to detect each of chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18 are each labeled with one or more independently detectable fluorophores to thereby enable correlation of the presence of signal from a particular fluorophore, or set of fluorophores, with the presence, absence and/or quantity of one of either chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 or 18.

e. Multiplex Assays:

In still another embodiment, this invention is directed to a multiplex assay suitable for detecting, identifying and/or enumerating at least two different human chromosomes in the same assay and in the same sample using at least two non-nucleic acid probes which are independently detectable. In preferred embodiments, each of the two or more probes can detect the presence, absenceand/or number of two of human chromosomes in the same sample and in the same assay. Preferably, the multiplex assay is a PNA-ISH or PNA FISH assay.

Examples 9 and 10 of this specification demonstrate the feasibility of multiplex fluorescent *in-situ* hybridization using independently detectable PNA probes. The Figures

which are to be viewed in connection with the description of these Examples conclusively demonstrate that individual human chromosomes are unambiguously detected in the sample wherein chromosomes X, Y and 1 are individually quantifiable both within the cells and the metaphase spreads.

f. Unique Multilabeled Non-Nucleic Acid Probes:

In still one more embodiment, this invention is directed to non-nucleic acid probes comprising two or more linked independently detectable moieties wherein the combination of the two or more linked independently detectable moieties is used to identify a particular probe/target sequence hybrid since the combination of the two or more linked moieties is unique. Preferably the independently detectable moieties are independently detectable fluorophores. The uniquely labeled non-nucleic acid probes are particularly well suited for use in a multiplex assay.

g. Exemplary Applications For Using The Invention:

Whether support bound or in solution, the non-nucleic acid probes, probe sets, methods and kits of this invention are particularly useful for the rapid, sensitive and reliable detection of human chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and/or 18. Thus, the non-nucleic acid probes, probe sets, methods and kits of this invention can be used to detect or identify chromosome related abnormalities. Non-limiting examples of chromosome related abnormalities which can be detected using this invention include aneuploidy karyotypes and polyploidy karyotypes. Additionally, the non-nucleic acid probes, probe sets, methods and kits of this invention are particularly useful for preimplantation diagnosis, for prenatal screening or for use in clinical diagnostic applications.

Having described the preferred embodiments of the invention, it will now become apparent to one of skill in the art that other embodiments incorporating the concepts described herein may be used. It is felt, therefore, that these embodiments should not be limited to disclosed embodiments but rather should be limited only by the spirit and scope of the following claims.

Examples:

This invention is now illustrated by the following examples which are not intended to be limiting in any way.

Example 1: Synthesis of bis-(2-methoxyethyl)amidyl-diglycolic acid

To 500 mmol of diglycolic anhydride stirring in 800 mL of dichloromethane (DCM) was added dropwise, 1.1 mole of bis(2-methoxyethyl)amine (Aldrich Chemical). The reaction was allowed to stir for 2 hours and then 280 mL of 6N HCl was added dropwise. The contents were then transferred to a separatory funnel and allowed to separate. The DCM layer was removed and the aqueous layer extracted with 100 mL of DCM. The combined DCM layers were then extracted with 100 mL of 10% aqueous citric acid. The DCM layer was then separated, dried (Na_2SO_4), filtered and evaporated to yield 73.8 g (296 mmole; 59 % yield). A kugelrorh was then used to remove traces of solvent (product was heated to 60 °C at approximately 180 μM Hg; but not distilled).

Example 2: Synthesis of N-[N''-Fmoc-(2''-aminoethyl)]-N-[N,N'-(2-methoxyethyl)amidyl-diglycolyl]glycine ("Fmoc-"E"aeg-OH")

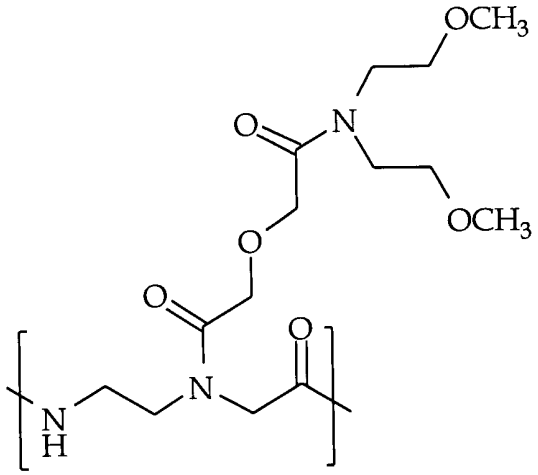
To 60 mmol of Fmoc-aeg-OH (PerSeptive Biosystems, Inc.) was added 360 mL of MilliQ water, 180 mL of acetone, 120 mmol of $NaHCO_3$ and 60 mmol of K_2CO_3. This solution was allowed to stir until all the Fmoc-aeg-OH had dissolved (approx. 2 hr.) and then the solution prepared, as described below, was added.

To 70 mmol of bis-(2-methoxyethyl)amidyl-diglycolic acid was added 120 mL of anhydrous acetonitrile (Fluka Chemical), 240 mmol of N-methylmorpholine (NMM; Fluka Chemical) and 75 mmol of trimethylacetyl chloride (Aldrich Chemical). The solution was allowed to stir at room temperature for 30 minutes and then added dropwise to the solution of Fmoc-aeg-OH which was prepared as described above.

After the combined solutions stirred for 1 hr and tlc analysis indicated complete reaction, 6N HCl was added to the reaction until the pH was less than 2 by paper. The organic solvent was then removed by vacuum evaporation. The remaining aqueous solution was then transferred to a separatory funnel and extracted 2 x with 250 mL of ethyl acetate. The combined ethyl acetate layers were dried (Na_2SO_4), filtered and evaporated to yield 41.5g of an oil.

This crude product was purified by column chromatography using a reversed phase stationary phase (C18) and a gradient of aqueous acetonitrile to elute the product and remove

the pivalic acid. Though not visible by tlc, the elution of the pivalic acid can be monitored by smell. The pivalic acid can be almost completely eluted from the column prior to elution of the product. Elution of the product can be monitored by tlc. Yield 26.8g (47 mmol; 78%). This "Fmoc-"E"aeg-OH" monomer was used directly on the PNA synthesis instrument, using standard condensation conditions, or used to prepare prederivatized synthesis supports which were used for the preparation of C-terminally "E" modified PNAs. An "E" modification (subunit) of a PNA or polyamide has the formula:



"E" subunit

Example 3: Synthesis of PNAs

Unless, otherwise stated, PNAs were synthesized using commercially available reagents and instrumentation obtained from PerSeptive Biosystems, Inc., Framingham, MA, USA. Double couplings were routinely performed to improve the quality of the crude products. PNAs possessing "E" modifications were prepared by performing the synthesis using prederivatized synthesis support or by performing the synthesis using Fmoc-"E"aeg-OH (prepared as described above) monomers. PNAs possessing C-terminal fluorescein (bis-fluorescein labeled PNAs) were prepared by performing the synthesis using the Fmoc-K(Mtt)-OH (Bachem, Torrance, CA, USA, P/N B-2535). Prior to performing the standard labeling procedure, the Mtt protecting group was removed using the following protocol.

The resin (still in the synthesis column) was treated with 10 mL of a solution containing 1% trifluoroacetic acid, 5% triisopropylsilane (TIS) in dichloromethane by passing the solution through the column over a period of approximately 15 minutes. After treatment, the synthesis support was washed with DMF. Prior to treatment with labeling reagent (See: Example 5), the

support was neutralized by treatment with approximately 10 mL of a solution containing 5% diisopropylethylamine in DMF.

Note: This procedure was only performed on PNA prepared using Fmoc-PAL-PEG/PS (PE Biosystems, Foster City, CA. P/N GEN913384). It was not performed with Fmoc-XAL-PEG/PS (PE Biosystems, Foster City, CA. P/N GEN913394).

Example 4: Preferred Method For Removal Of The Fmoc Protecting Group

The synthesis support was treated with a solution of 25% piperidine in DMF for 10-15 minutes at room temperature. After treatment, the synthesis support was washed and dried under high vacuum. The support can then be treated with labeling reagent (See: Example 5).

Example 5: Preferred Method For Amine Labeling of Support Bound PNA with the NHS esters of 5(6)carboxyfluorescein (Flu) or 5(and 6)-carboxy-X-rhodamine (Rox)

The amino protecting group (Fmoc) of the assembled PNA was removed and the synthesis support was washed and dried under vacuum. The synthesis support was then treated for 4-5 hours at 30-37 °C with approximately 250 µL of a solution containing 0.08 M NHS ester labeling reagent, 0.24 M DIEA and 0.24 M 2,6-lutidine. After treatment the synthesis support was washed and dried under high vacuum. The PNA oligomer was then cleaved, deprotected and purified.

Example 6: General Procedure For Labeling Of Support Bound PNA With 5(6)carboxyfluorescein

After proper reaction with linkers and removal of the terminal amine protecting group, the resin was treated with 250 µL of a solution containing 0.5M 5(6)carboxyfluorescein, 0.5M N,N'-diisopropylcarbodiimide, 0,5M 1-hydroxy-7-azabenzotriazole (HOAt) in DMF (See: Weber et al., *Bioorganic & Medicinal Chemistry Letters, 8:* 597-600 (1998). After treatment the synthesis support was washed and dried under high vacuum. The PNA oligomer was then cleaved, deprotected and purified as described below.

Note on Fluorescein Labeling: The fluorescein labeled PNAs described herein were prepared using several different procedures. The different procedures have evolved to optimize

fluorescein labeling conditions. At this time we prefer to use the procedure of Weber et al. for most fluorescein labeling operations.

Example 7: General Procedure For Cleavage, Deprotection and Purification

The synthesis support (Fmoc-PAL-PEG/PS; P/N GEN913384) was then removed from the synthesis cartridge, transferred to a Ultrafree spin cartridge (Millipore Corp., P/N SE3P230J3) and treated with a solution of TFA/m-cresol (either of 7/3 or 8/2 (preferred)) for 1-3 hours. The solution was spun through the support bed and again the support was treated with a solution of TFA/m-cresol for 1-3 hours. The solution was again spun through the support bed. The combined eluents (TFA/m-cresol) was then precipitated by addition of approximately 1 mL of diethyl ether. The precipitate was pelletized by centrifugation. The pellet was then resuspended in ethyl ether and pelletized two additional times. The dried pellet was then resuspended in 20% aqueous acetonitrile (ACN) containing 0.1 % TFA (additional ACN was added as necessary to dissolve the pellet). The product was analyzed and purified using conventional reversed phase chromatographic methods.

Note: Several PNAs were prepared using new product Fmoc-XAL-PEG/PS synthesis support (P/N GEN 913394) available from PerSeptive. This support has the advantage that the PNA can be removed more rapidly and under more mildly acid conditions. For PNAs prepared with Fmoc-XAL-PEG/PS the support is treated as described above except that a solution of TFA/m-cresol 9/1 was used for a period of 10-15 minutes (2x).

Example 8: Cy5 Labeling of PNAs

The purified amine containing PNA was dissolved in 1/1 DMF/water at a concentration of approximately 0.05 OD/μL to prepare a stock PNA solution. From the stock, approximately 30 nmole of PNA was added to a tube. To this tube was then added 125 μL 0.1 M HEPES (pH 8.5), and enough 1/1 DMF/water to bring the total volume to 250 μL. This solution was thoroughly mixed. To a prepackaged tube of Cy5 dye (Amersham P/N PA-25001), was added the entire 250 μL solution prepared as described above. The tube was well mixed and then allowed to react for 1 hour at ambient temperature.

After reaction, the solvent was removed by evaporation in a speed-vac. The pellet was then dissolved in 400 μL of a solution containing 3:1 1 % aqueous TFA/ACN. Optionally the solution was then transferred to a 5000 MW Ultrafree (Millipore, P/N UFC3LCC25) or a 3000

MW (Amicon, P/N 42404) filter to removed excess dye. The recovered product was then repurified using reversed phase chromatographic methods.

Example 9: PNA-FISH Used For The Detection Of Human Chromosomes X, Y, 1, 2, 3, 6, 8, 10, 11, 12, 16, 17 and 18

PNA Oligomers Prepared:

Table 2

Probe ID	Target Human Chromosome	PNA Probe Sequence
Rox-X-I	X	Rox-OE-CTT-CAA-AGA-GGT-CCA-CGA-E-NH_2
Rox-X-II	X	Rox-OEE-AGG-GTT-CAA-CTG-TGT-GAC-E-NH_2
Rox-X-III	X	Rox-OEE-GAA-ACT-TCT-GAG-TGA-TGA-EE-NH_2
Rox-X-VI	X	Rox-OEE-CAG-TCA-TCG-CAG-AAA-ACT-EE-NH_2
Rox-X-V	X	Rox-OEE-AGA-TTT-CAC-TGG-AAA-CGG-EE-NH_2
Rox-X-VI	X	Rox-OEE-GTT-ATG-GGA-AGG-TGA-TCC-EE-NH_2
Rox-X-VII	X	Rox-OEE-TCG-AGC-CGC-AGA-GTT-TAA-EE-NH_2
Rox-X-VIII	X	Rox-OEE-CTA-TTT-AGC-GGG-CTT-GGA-EE-NH_2
Rox-X-IX	X	Rox-OEE-TAC-AAG-GGT-GTT-GCA-AAC-EE-NH_2
Flu-Y-I	Y	Flu-OE-CCA-TAT-GCA-GTT-ATA-AGT-AGG-E-NH_2
Flu-Y-II	Y	Flu-OE-TAT-TGT-ACC-AAG-CAG-AGT-ACC-E-NH_2
Flu-Y-III	Y	Flu-OEE-GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA-EE-NH_2
Flu-Y-IV	Y	Flu-OEE-GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT-EE-NH_2
Flu-Y-V	Y	Flu-OEE-TCA-CAT-AAT-AGA-CAA-CAT-AC-EE-NH_2
Flu-Y-VI	Y	Flu-OEE-CAG-AAG-AGA-TTG-AAC-CTT-EE-NH_2
Flu-Y-VII	Y	Flu-OEE-GGC-ATA-GCA-CAT-AAC-ATG-EE-NH_2
Rox-1-I	1	Rox-OE-AAT-CGT-CAT-CGA-ATG-AAT-E-NH_2
Rox-1-II	1	Rox-OE-CAT-TGA-ACA-GAA-TTG-AAT-E-NH_2
Cy5-1-I	1	Cy5-OE-AAT-CGT-CAT-CGA-ATG-AAT-E-NH_2
Cy5-1-II	1	Cy5-OE-CAT-TGA-ACA-GAA-TTG-AAT-E-NH_2
Flu-2-I	2	Flu-OEE-GTT-TTC-AGG-GGA-AGA-TAT-EEO-K(Flu)-NH_2
Flu-2-II	2	Flu-OEE-TGT-GCG-CCC-TCA-ACT-AAC-EEO-K(Flu)-NH_2
Flu-2-III	2	Flu-OEE-GAA-GCT-TCA-TTG-GGA-TGT-EE-NH_2
Flu-2-IV	2	Flu-OEE-CCA-ATA-AAA-GCT-ACA-TAG-A-EEO-K(Flu)-NH_2
Flu-2-V	2	Flu-OEE-GAA-AAA-GTT-TCT-GAC-ATT-GC-EE-NH_2
Flu-2-VI	2	Flu-OEE-TAG-TTG-AAG-GGC-ACA-TCA-EE-NH_2
Flu-2-VII	2	Flu-OEE-CAC-AAA-TAA-GAT-TCT-AAG-AAT-EE-NH_2
Flu-2-VIII	2	Flu-OEE-TCA-AAA-GAA-TGC-TTC-AAC-AC-EE-NH_2
Rox-3-I	3	Rox-OEE-ATA-ATT-AGA-CCG-GAA-TCA-T-E-NH_2
Rox-3-II	3	Rox-OEE-GCT-GTT-TTC-TAA-AGG-AAA-G-EE-NH_2
Rox-3-III	3	Rox-OEE-AAG-ACT-TCA-AAG-AGG-TCC-E-NH_2
Flu-3-I	3	Flu-OEE-TTT-GTC-AAG-AAT-TAT-AAG-AAG-EE-NH_2
Flu-3-II	3	Flu-OEE-CAA-GAT-TGC-TTT-TAA-TGG-EE-NH_2
Flu-3-III	3	Flu-OEE-TGT-GTA-TCA-ACT-CAC-GGA-EE-NH_2

Flu-3-IV	3	Flu-OEE-CCT-CAC-AAA-GTA-GAA-ACT-EE-NH_2
Flu-3-V	3	Flu-OEE-GAA-AAA-GCA-GTT-ACT-GAG-EE-NH_2
Flu-3-VI	3	Flu-OEE-TAA-TAA-TTA-GAC-GGA-ATC-AT-EE-NH_2
Flu-3-VII	3	Flu-OEE-TTA-CAG-GGC-ATT-GAA-GCC-EE-NH_2
Flu-3-VIII	3	Flu-OEE-CAG-TTA-TGA-AGC-AGT-CTC-EE-NH_2
Flu-3-IX	3	Flu-OEE-CAC-ACC-AGA-AAA-AGC-AGT-EE-NH_2
Flu-3-X	3	Flu-OEE-AAG-GGT-AAA-CAC-TGT-GAG-EE-NH_2
Flu-3-XI	3	Flu-OEE-AGA-CAA-CGA-AAT-ATC-TTC-ATG-EE-NH_2
Flu-3-XII	3	Flu-OEE-CTA-GCA-GTA-TGA-GGT-CAA-EE-NH_2
Flu-3-XIII	3	Flu-OEE-GCA-GAC-TTC-AGA-AAC-AGA-EE-NH_2
Flu-3-XIV	3	Flu-OEE-GGC-CTC-AAA-GAC-GTT-TAA-EE-NH_2
Flu-3-XV	3	Flu-OEE-GTG-AAA-GTT-CCA-AGT-GAA-EE-NH_2
Flu-3-XVI	3	Flu-OEE-GAG-TGC-TTT-GAA-GCC-TAC-EE-NH_2
Flu-3-XVII	3	Flu-OEE-GAA-ACA-GCA-GAG-TTG-AAA-EE-NH_2
Flu-3-XVIII	3	Flu-OEE-TGC-AGA-GAT-CAC-AAC-GTG-EE-NH_2
Flu-3-XIX	3	Flu-OEE-ACA-AAG-AAT-CAT-TCG-CAG-EE-NH_2
Flu-3-XX	3	Flu-OEE-AGT-GTT-AGA-AAA-CTG-CTC-EE-NH_2
Flu-6-I	6	Flu-OEE-CTG-TTC-AGA-GTA-ACA-TGA-EE-NH_2
Flu-6-II	6	Flu-OEE-CCG-CTT-GGA-AAT-ACT-ACA-EE-NH_2
Flu-6-III	6	Flu-OEE-GAA-ATG-GAA-ATA-TCT-CCC-C-E-NH_2
Flu-6-IV	6	Flu-OEE-TCT-AGG-AGG-TCC-AAT-TAT-E-NH_2
Flu-6-V	6	Flu-OEE-GAA-TTC-CCA-AGT-GGA-TAT-EE-NH_2
Flu-6-VI	6	Flu-OEE-CTG-TAG-GTT-TAG-ATG-AAG-EE-NH_2
Flu-6-VII	6	Flu-OEE-AAG-GAG-TGT-TTC-CCA-ACT-EE-NH_2
Flu-6-VIII	6	Flu-OEE-GGC-TTC-AAG-GCG-CTC-TAA-EE-NH_2
Flu-6-IX	6	Flu-OEE-GCA-GAG-ACT-TCA-AAG-TGC-EE-NH_2
Flu-6-X	6	Flu-OEE-CAC-ACA-CAC-GGT-GGA-CCA-E-NH_2
Flu-6-XI	6	Flu-OEE-CAA-AGG-GAA-TGT-TCC-ATT-EE-NH_2
Flu-6-XII	6	Flu-OEE-CAC-ATA-GCA-GTG-TTT-GAG-EE-NH_2
Flu-6-XIII	6	Flu-OEE-CTC-AAG-GCG-GTC-CAA-TTA-E-NH_2
Flu-6-XIV	6	Flu-OEE-GAG-TCG-AAA-TGC-ACA-CAT-E-NH_2
Flu-6-XV	6	Flu-OEE-TAC-CAA-GAG-GAA-TGT-TGC-EE-NH_2
Rox-8-I	8	Rox-OE-ACG-GGA-TGC-AAT-ATA-AAA-E-NH_2
Rox-8-II	8	Rox-OE-TGA-AGA-TTC-TGC-ATA-CGG-E-NH_2
Rox-8-III	8	Rox-OE-AAG-GTT-TGT-ACT-GAC-AGA-E-NH_2
Rox-8-IV	8	Rox-OE-CTG-AAC-TAT-GGT-GAA-AAA-E-NH_2
Rox-8-V	8	Rox-OE-ACT-AAC-TGT-GCT-GAA-CAT-E-NH_2
Rox-8-VI	8	Rox-OE-CCC-ATG-AAT-GCG-AGA-TAG-E-NH_2
Rox-10-I	10	Rox-OEE-AAC-TGA-ACG-CAC-AGA-TGA-EE-NH_2
Rox-10-II	10	Rox-OEE-GGC-TAA-TCT-TTG-AAA-TTG-AAA-EE-NH_2
Rox-10-III	10	Rox-OEE-AGG-TGG-ATA-ATT-GGC-CCT-EE-NH_2
Rox-10-IV	10	Rox-OEE-TGA-AGT-CCA-AAA-AAG-CAC-EE-NH_2
Rox-10-V	10	Rox-OEE-CTT-AGA-CAT-GGA-AAT-ATC-E-NH_2
Rox-10-VI	10	Rox-OEE-AAG-GGG-TCT-AAC-TAA-TCA-E-NH_2
Flu-10-VII	10	Flu-OEE-GTA-GTT-GTT-GAG-AAT-GAT-EE-NH_2
Rox-11-I	11	Rox-OEE-AAC-TTC-CCA-GAA-CTA-CAC-EE-NH_2
Rox-11-II	11	Rox-OEE-ATT-CTT-GAA-ATG-GAA-CAC-EE-NH_2

Rox-11-III	11	Rox-OEE-CTG-TGA-TTG-CTG-ATT-TGG-EE-NH_2
Rox-11-IV	11	Rox-OEE-GTC-ATC-ACA-GGA-AAC-ATT-EE-NH_2
Rox-11-V	11	Rox-OEE-GAA-ATT-TCC-TGT-TGA-CAG-A-EE-NH_2
Flu-11-I	11	Flu-OEE-GTT-TGA-AAG-CTG-AAC-TAT-G-E-NH_2
Flu-12-I	12	Flu-OEE-TCC-TGT-AAT-GTT-CGA-CAG-EE-NH_2
Flu-12-II	12	Flu-OEE-TCA-TAG-AAC-GCT-AGA-AAG-EE-NH_2
Flu-12-III	12	Flu-OEE-ACC-TTT-CTT-TTG-ATG-AAG-GA-EE-NH_2
Flu-12-IV	12	Flu-OEE-CAA-ATA-TCA-CAA-AAA-GAG-GG-EE-NH_2
Flu-12-V	12	Flu-OEE-GAG-TTG-AAT-AGA-GGC-AAC-EE-NH_2
Flu-12-VI	12	Flu-OEE-GGC-CAA-ATG-TAG-AAA-AGG-EE-NH_2
Flu-12-VII	12	Flu-OEE-GCG-TTC-AAC-TCA-AGG-TGT-EE-NH_2
Flu-12-VIII	12	Flu-OEE-TGT-CCT-TTA-GAC-AGA-GCA-EE-NH_2
Flu-12-IX	12	Flu-OEE-TGA-GAC-CAA-ATG-TAC-AAA-AG-EE-NH_2
Flu-12-X	12	Flu-OEE-GAA-TAC-TGA-GTA-AGT-TCT-TTG-EE-NH_2
Flu-12-XI	12	Flu-OEE-AAC-TGC-ACA-AAT-AGG-GTG-EE-NH_2
Flu-12-XII	12	Flu-OEE-TGG-AGA-CAC-TGT-GTT-TGT-E-NH_2
Flu-12-IX	12	Flu-OEE-CCA-GTT-GGA-GAT-TTC-AAT-E-NH_2
Flu-16-I	16	Flu-OE-GAA-GCC-TGC-CAG-TGG-ATA-E-NH_2
Flu-16-II	16	Flu-OE-TAC-AGC-ATT-CTG-GAA-ACC-E-NH_2
Rox-16-I	16	Rox-OE-CCA-GAC-ACT-GCG-TAG-TGA-E-NH_2
Rox-16-II	16	Rox-OE-ATA-TAA-TGC-TAG-AGG-GAG-E-NH_2
Rox-16-III	16	Rox-OE-AAA-AAC-AAG-ACA-AAC-TCG-E-NH_2
Flu-17-I	17	Flu-OE-ATT-TCA-GCT-GAC-TAA-ACA-E-NH_2
Flu-17-II	17	Flu-OE-AAC-GAA-TTA-TGG-TCA-CAT-E-NH_2
Flu-17-III	17	Flu-OE-GGT-GAC-GAC-TGA-GTT-TAA-E-NH_2
Flu-17-IV	17	Flu-OEE-TTT-GGA-CCA-CTC-TGT-GGC-EE-NH_2
Flu-17-V	17	Flu-OEE-AAC-GGG-ATA-ACT-GCA-CCT-EE-NH_2
Flu-17-VI	17	Flu-OEE-TTT-GTG-GTT-TGT-GGT-GGA-EE-NH_2
Flu-17-VII	17	Flu-OEE-AGG-GAA-TAG-CTT-CAT-AGA-EE-NH_2
Flu-17-VIII	17	Flu-OEE-ATC-ACG-AAG-AAG-GTT-CTG-EE-NH_2
Flu-17-XI	17	Flu-OEE-CCG-AAG-ATG-TCT-TTG-GAA-EE-NH_2
Flu-17-X	17	Flu-OEE-AAA-GAG-GTC-TAC-ATG-TCC-EE-NH_2
Flu-18-I	18	Flu-OEE-TTC-CCG-TAA-CAA-CTA-TGC-EE-NH_2
Flu-18-II	18	Flu-OEE-TCC-CGT-AAC-AAC-TAG-GCA-EE-NH_2
Flu-18-III	18	Flu-OEE-AAA-AGG-AGT-GAT-CCA-ACC-EE-NH_2
Flu-18-IV	18	Flu-OEE-TCC-CTT-TGG-TAG-AGC-AGG-EE-NH_2
Flu-18-V	18	Flu-OEE-ATT-TGA-GAT-GTG-TGT-ACT-CA-EE-NH_2
Flu-18-VI	18	Flu-OEE-GCA-CTT-ACC-GGC-CTA-AG-EE-NH_2
Flu-18-VII	18	Flu-OEE-CTC-AGA-AAC-TTA-CTC-GTG-EE-NH_2

PNA sequences are written from the amine (N-) terminus to the carboxyl (C-) terminus. K= the amino acid L-lysine; Flu = 5(6)-carboxyfluorescein; Rox = 5(and 6)-carboxy-X-rhodamine; Cy5 is the cyanine 5 dye obtained from Amersham/Pharmacia; O = 8-amino-3,6-dioxaoctanoic acid and "E" has been previously described herein.

Preferred Method For Cytogenetic Preparations:

Human normal or patient cells were incubated in culture with 0.015μg/mL colcemid for 45-60 min (Taneja et al., *The Journal of Cell Biology, 12*: 995-1002 (1995)). After incubation, media was removed in a 50 mL centrifuge tube. In case of fibroblast or attached cells, the cells were trypsinized with 0.5% trypsin-EDTA in Hank's Balanced Salt Solution (HBSS, Gibco, BRL). Trypsinized cells were added to the previously removed media to stop the trypsin reaction. Cells were then centrifuged at approximately 1000 rpm for 5 min and the cell pellet was resuspended in 10 mL of 0.075M KCl. Cells were incubated at 37°C for 15 min, and again centrifuged at approximately 1000 rpm for 5 min. Ten milliliters of freshly prepared methanol/acetic acid (3:1) was then added drop by drop with mixing to the cell pellet. The cells were thereafter incubated at room temperature for 10 min and again centrifuged. Approximately 10 mL of methanol/acetic acid (3:1) was again added to the cells and then the cells were incubated for 10 min at room temperature. Cells were then centrifuged, the supernatant was removed, and the cell pellet resuspended in 1 mL of methanol/acetic acid (3:1). Cells were dropped onto ethanol washed slides and dried in air overnight. Finally, slides were incubated at 65°C for one hour and stored at -80°C.

Design of Chromosome Specific Probes:

Probes for X chromosome were designed from the clone pBamX7 of DXZ1 locus (Waye et al., *Nucl. Acids Res., 13*: 2731-2743 (1985)) and were labeled with rhodamine (red). The pBamX7 clone is 2 kb alpha satellite DNA which hybridized to 5000 copies located in the centromeric region of X chromosome (Willard et al., 1986; *The Journal of Cell Biology* et al., 1987). Probes for the Y chromosome were designed from 2.47 kb repeat sequences in DYZ2 locus (Frommer M., et al., 1984). The human Y chromosome carries 2000 copies of tandemly repeat sequences (a 2.47 kb fragment) and localized on the long arm of the Y chromosome (Cooke et al., *Chromosoma (Berl.) 87*: 491-502 (1982)). PNA probes for detecting the human Y chromosome were labeled with fluorescein (green). Chromosome 1 specific PNA probes were derived from the published human satellite 2 sequences (Jeanpierre M., *Ann. Genet, 37*: 1994). Satellite 2 DNA is present in the pericentric heterochromatin region on the long arm of chromosome 1 (1q12). Chromosome 1 specific probes were labeled with rhodamine or Cy5. Table 1 lists only those probing nucleobase sequences which, when tested in hybridizations assays, were found to be specific for the chromosomes sought to be detected. The target sequences for the chromosome specific probing nucleobase sequences (18-23 bases) listed in Table 1, were checked for cross

hybridization using sequence alignment analysis. Probes for human chromosome 2 were designed from p2-11 (See: Haaf and Willard, *Genomics, 13:* 122-128 (1992)) and were labeled with fluorescein (green). The clone p2-11 is 1356 bp long and is part of the D2Z1 locus. The D2Z1 array spans about 1050-2900kb of the centromere of chromosome 2. Probes for human chromosome 3 were designed from Gene Bank accession number M29460 (HS3ALPH, Smith et al., unpublished), M29461 (HS6ALPH, Smith et al., unpublished), and X06394 (HSREPA18, Delattre et al., *Nucleic Acid Research, 15:* 8561 (1987)) and were labeled with fluorescein. The clones (HS3ALPH (345 bp), HS6ALPH (676 bp) and HSREPA18 (635 bp)) are the part of alpha satellite sequences and localized at the centromere of chromosome 3. Probes for human chromosome 6 were designed from clone 308 (See: Jabs and Persico, *Am. J. Hum. Genet, 41:* 374-390 (1987)) and were labeled with fluorescein (green). The clone 308 is a 2.9 kb Bam HI DNA fragment of higher order repeat unit consisting of 19 alphoid monomers. It is a part of D6Z1 locus and is located in the centromere of chromosome 6. Chromosome 8 specific probes were taken from the gene Bank accession number M64779 (HSD8Z2AA, Ge et al., unpublished), originated from chromosome 8 and is a part of D8Z2 locus. The target to these probes is present on the centromere of chromosome 8. Probes for human chromosome 10 were designed from the centromeric probe pα10RP8, a 912 bp clone in the D10Z1 locus (Howe et al., *Hum. Genet., 91:* 199-204 (1993)), and were labeled with either fluorescein (green) or rhodamine (red). The pα10RP8 fragment is located in the centromeric region of chromosome 10. The principle repetitive unit of this alpha satellite subset is an 850 bp XbaI fragment (clone pLC11A, Waye et al., *Chromosoma, 95*: 182-188 (1987)) composed of five tandem diverged alphoid monomers; each of ~ 171 bp in length. The pentamer repeat units are themselves tandemly reiterated in ~ 500 copies per chromosome 11. These probes were specific for the centromeric alpha satellite sequences of chromosome 11. Chromosome 12 specific probes were taken from clone pGR12 (D12Z3). A 685 bp fragment of alpha satellite DNA sequences, (Gene Bank accession number M28221 (Rocchi et al., *Am. J. of Hum. Genet. 46*: 784-788, 1990)), originated from the chromosome 12 centromere. Probes for human chromosome 16 were designed from pSE-16-2 (See: Greig et al., *Am. J. Hum. Genet., 45*: 862-872 (1989)) and were labeled with either fluorescein (green) or rhodamine (red). The clone pSE-16-2 is 340 bp long and is part of the D16Z2 locus. The D16Z2 array spans about 1400-2000 kb of the centromere of chromosome 16. Probes for human chromosome 17 were designed from p17H8 (See: Waye et al, *Molecular and Cellular Biology, 6:* 3156-3165 (1986)) and were labeled with fluorescein (green). The clone p17H8 is a 2.7 kb higher order repeat unit consisting of 16 alphoid monomers, which is 500-1000 copies located in the

centromere of chromosome 17. Probes for human chromosome 18 were designed from the 1360 bp pst-1 insert of pYAM9-60 in the D18Z1 locus (Alexandrov et al., *Genomics 11:* 15-23 (1991)) and were labeled with either fluorescein (green). The pYAM9-60 fragment is located in the centromeric region of chromosome 18.

PNA probes for a particular chromosome listed in Table 2 used in a particular experiment were first mixed before hybridization with the cells.

Preferred Procedure For Performing *In-Situ* Hybridization:

Slides containing interphase nuclei and metaphase chromosome spreads, prepared as described above were treated with 25 µL of hybridization buffer (70% formamide, 1x Denhardt solution, 10 mM NaCl, 20 mM Tris pH 7.5 , 0.1 µg/mL each of E. Coli tRNA and salmon sperm DNA) containing 0.1 pM of each fluorochrome labeled PNA probe for a particular chromosome listed in Table 2 (Except for X, Y and 1: See note below for information on probes used to generate the Figures). Slides were then heated at 70°C for 10 minutes in a humidified incubator and then transferred to a ambient humidified incubator and PNA probe hybridization was allowed to proceed for 30-60 minutes. After a brief rinse in PBS and 0.1% tween 20 (Sigma) at room temperature, slides were washed in preheated 0.1% tween 20 in PBS (PBS is 2.7 mM KCl, 1.5 mM KH_2PO, 137 mM NaCl, and 8 mM Na_2HPO) at 55°C for 30 minutes. Finally the slides were rinsed with PBS. Slides were then dehydrated in 70% and 100% ethanol for two minutes each and air dried for 10 minutes. Cells were then counterstained with 4,6-diamino-2-phenylindole (DAPI, Sigma Chemicals) and were mounted in 1,4-phenylenediamine in 90% glycerol in PBS. Slides were then analyzed using a microscope equipped with a CCD digital camera.

Digital Imaging Microscopy:

Images reproduced in Figures 1-11 and 13-16 were obtained using a Nikon fluorescent microscope equipped with a 60 x immersion oil objective, a 10 x ocular (total enlargement is 600 fold) and light filters obtained from Omega Optical (XF22 (green), XF34 (red), and XF05 (blue) filter). Electronic digital images were made of the slide using a SPOT CCD-camera and software obtained from Diagnostic Instruments, Inc., Sterling Heights, MI (USA).

Results:

General:

The composite digital images obtained, all covering the same section of the slide, are presented in Figures 1-11 and 13-16. With reference to the color images of Figures 1-11 and 13-

16, the blue Dapi stain was used to visualize chromosomes of the metaphase spreads and interphase nuclei.

Specific Figures:

General Note: The Cy5 labeled probes listed in Table 2 were not used to generate any of Figures 1-11, 13-16. Figures 1-5 were obtained with only probes Rox-X-I-III and Flu-Y-I-IV and not probes of the entire set as identified in Table 2.

Figure 1: Chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of chromosomes indicate that these cells come from a normal human male.

Figure 2: Chromosomes X and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of chromosomes indicate that these cells come from a normal human female (chromosome Y was not detected).

Figure 3: Chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The imbalance in detectable chromosomes indicates that these cells come from human having an additional Y-chromosome (47XYY). This is an aneuploidy condition known as trisomy.

Figure 4: Chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. The imbalance in detectable chromosomes indicates that these cells come from human having three additional X-chromosomes (49XXXXY). This is an aneuploidy condition known as pentasomy.

Figure 5: Metaphase chromosomes of a human having a condition known as triploid (polyploidy) 69XXY is clearly detectable. It is noteworthy that without having the chromosome 1 reference (3 copies of chromosome 1 is visible), it would be more difficult to properly diagnosis this patent as polyploidy as compared with an aneuploidy 47XXY karyotype.

Figure 6: Pairs of human chromosome 2 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of white spots indicate that these cells come from a human having a pair of human chromosome 2.

Figure 7: Pairs of human chromosome 6 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of human chromosome 6.

Figure 8: Pairs of chromosome 10 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of human chromosome 10.

Figure 9: Pairs of chromosome 16 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of white spots indicate that these cells come from a human having a pair of chromosome 16.

Figure 10: Pairs of chromosome 17 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of chromosome 17.

Figure 11: Pairs of chromosome 18 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of chromosome 18.

Figure 13: Pairs of chromosome 3 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of chromosome 3.

Figure 14: Pairs of chromosome 8 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of chromosome 8.

Figure 15: Pairs of chromosome 11 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of chromosome 11.

Figure 16: Pairs of chromosome 12 are clearly detectable in the visible interphase nuclei and metaphase spreads. The perfectly paired sets of green spots indicate that these cells come from a human having a pair of chromosome 12.

Example 10: Multiplex PNA-FISH Used For The Independent Detection Of Human Chromosomes X, Y and 1

Cytogenetic Preparations:

Cells were prepared essentially as described in Example 9.

Preparation of Chromosome Specific Probes:

Probe Design is essentially as described in Example 9.

Specific PNA probes used to generate Figure 12 are listed in Tables 2 except that probes Cy5-1-I and Cy5-1-II were substituted for Rox-1-I and Rox-1-II, respectfully. Therefore, all of the

PNA probes for chromosomes X, Y and 1 listed in Table 2 (except for Rox-1-I and Rox-1-II) were mixed before hybridization with the cells prepared as described under subheading "Cytogenetic Preparations".

In-Situ Hybridization:

In-Situ Hybridization, using the mixture of PNA probes was performed essentially as described in Example 9.

Digital Imaging Microscopy:

The image reproduced in Figures 12 was obtained essentially as described in Example 9, except that light filters were as follows: The filter sets for green (XF22), red (XF34), blue (XF05) were obtained from Omega Optical. The filter set for the Cy5 dye (P/N 31023, Ex: D640/20 and Em: D680/30) was obtained from Chroma Technology Corp. However, the colors appearing in the figure have been pseudocolored (by the software) since Cy5 is not visible. The green and blue filter sets still yields a green and blue signal, respectfully. However, the red filter set has fixed to appear as pseudocolor orange (identifies the rhodamine labeled X chromosome probe) in the Figure and the Cy5 filter set has been fixed to appear as pseudocolor red in the Figure.

Results:

General:

The composite digital image obtained, all covering the same section of the slide, are presented in Figures 12A and 12B. With reference to the Figures, the blue Dapi stain was used to visualize chromosomes of the metaphase spreads and interphase nuclei. The signal from the CCD camera for each filter set was colored or pseudocolored using the software. Colors presented in the Figure are pseudocolor orange (chromosomes X), green (chromosomes Y) and pseudocolor red Cy5 (Chromosomes 1). Because the multicolor analysis provides a means to identify the sex chromosomes (X and Y) as well as a reference chromosome (chromosome 1), it is possible to detect chromosome abnormalities associated with both aneuploidy and polyploidy conditions.

Specific Figures:

Figure 12A: Chromosomes X and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. In the Figure, each individual X, Y and 1 chromosome can be detected and counted (scored) since three independently detectable fluorophores were used, one for each chromosome type. The data indicates that these cells come from normal human female (XX).

Figure 12B: Chromosomes X, Y and 1 are clearly detectable in the visible interphase nuclei and metaphase spreads. In the Figure, each individual X, Y and 1 chromosome can be detected and

counted (scored) since three independently detectable fluorophores were used, one for each chromosome type. The data indicates that these cells come from a normal human male.

EQUIVALENTS

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those of ordinary skill in the art that various changes in form and details may be made therein without departing from the spirit and scope of the invention as defined by the appended claims. Those skilled in the art will be able to ascertain, using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed in the scope of the claims.